582	950	611	844	-230	589	182	637	609
10	672	3	680	87	2	102	125	475
100%	%96	100%	95% 100%	41.2	100%	100%	100%	70.5
Q9Y691	Q9GZR7	890H6Ò	беер9	PF01758	О96ЕР9	AAH08044	FXY5_HUMAN	PF02038
(Q9Y691) MAXIK CHANNEL BETA 2 SUBUNIT (LARGE CONDUCTANCE CALCIUM-ACTI	(Q9GZR7) HYPOTHETICAL 96.3 KDA PROTEIN (ATP- DEPENDENT RNA HELICASE) ((Q9H068) HYPOTHETICAL 69.9 KDA PROTEIN.	(Q96EP9) Unknown (protein for IMAGE:3502817) (Fragment).	PFAM: Sodium Bile acid symporter family	(Q96EP9) Unknown (protein for IMAGE:3502817) (Fragment).	(AAH08044) Unknown (protein for MGC:16063).	(Q96DB9) FXYD domain-containing ion transport regulator 5 p	PFAM: ATP1G1/PLM/MAT8
WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64	HMMER 2.1.1
51	53	54	56	646		647	28	648
748244	625916	843036	1352403	1045580		1027748	1352412	1094642
HATCP77	HBAFJ33	HBAFV19	HBCPB32	НВСРВ32		HBCQL32	HBGNU56	HBGNU56

				family				
			┿	(Q96DB9) FXYD	FXY5_HUMAN	100%	62	612
			.64	domain-containing ion				
				transport regulator 5 p				,
HBGNU56	1050255	649		PFAM:	PF02038	70.5	521	655
			2.1.1	ATP1G1/PLM/MAT8				
				family				
			WUblastx	(Q96DB9) FXYD	FXY5_HUMAN	100%	125	959
			.64	domain-containing ion				
				transport regulator 5 p				
HBHMA23	848016	09	WUblastx	(AAM00283) Von Ebner	AAM00283	100%	643	1035
			.64	minor protein.		%66	71	649
HRHMA23	699815	650	WUblastx	1	AAM00283	100%	70	273
))	.64			%26	907	1032
						%16	641	916
						64%	261	647
HBIMB51	963208	61	WUblastx	(Q969E3) Urocortin III	Q969Е3	%66	86	535
			.64	(Stresscopin).		7007	700	2.73
HBIMB51	672711	651	WUblastx .64	(Q924A4) Urocortin III.	Q924A4	61% 64%	296 93	302
HBINS58	1352386	62	WUblastx	(Q9D6W7)	7W9Ф6Ф	81%	57	278
			.64	2310047N01RIK PROTEIN.				
HBINS58	961712	652	WUblastx	(Q9D6W7)	Q9D6W7	%08	71	589
			j.	PROTEIN.				
HBINS58	892924	653	WUblastx	L	7W9Q6Q	%62	100	579
			+ •					
HBJFU48	460392	63	WUblastx	(Q9P195) PRO1722.	Q9P195	63%	716	099

718	533	891	070	740			008				245		907		786	C	86/				908					340		000	807
819	299	223	177	133		,	99	-			144		77		409		40	-			57			-		128			53
73%	64%	131.8	/000	93%			100%				30.1		%6L		250.2		100%				75%	_				45.4			100%
		PF00335		AAH24685			pir S14350 C1HUQA				PF01391		Q9H2L7		PF00386		pir S14350 C1HUQA	~			076076			-		PF00219			076076
		: Transmembrane 4	Taliniy	(AAH24685) Similar to	transmembrane 4	superfamily m	complement	subcomponent C1q chain	A precursor [validated] -	human	PFAM: Collagen triple	helix repeat (20 copies)	(Q9H2L7) DC33.		PFAM: C1q domain		complement	subcomponent C1q chain	A precursor [validated] -	human	(076076) CONNECTIVE	TISSUE GROWTH	FACTOR-LIKE	PROTEIN PRECURSOR	(BA44	PFAM: Insulin-like	growth factor binding	proteins	(076076) CONNECTIVE
64	<u> </u>	HMMER	2.1.1	WUblastx	.64		WUblastx	.64			HMMER	2.1.1	WUblastx	.64	HMMER	2.1.1	WUblastx	.64			WUblastx	.64				HMMER	2.1.1		WUblastx
		99					89				654				655						71					959			
		732111				•	1125802				899397				902207						1300752					1121709			
		HBJLF01					HBJNC59				HBJNC59				HBJNC59						HB0EG11					HB0EG11			

	334	796	314	1008	820	1009	312 1015	525 592 683
	122	47	424 345	4	548	8	323	590 645 859
	45.4	100%	71%	%66	%69	85%	%16 %16	86% 61% 65%
	PF00219	076076	Q9NS11	Q8WYF7	Q9NX85	6М166О	Q96BN2	Q9NX85
TISSUE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (BA44	PFAM: Insulin-like growth factor binding proteins	(076076) CONNECTIVE TISSUE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (BA44	(Q9NS11) LIPOPOLYSACCHARID E SPECIFIC RESPONSE- 68 PROTEIN.	(Q8WYF7) POB1.	(Q9NX85) CDNA FLJ20378 FIS, CLONE KAIA0536.	(Q99LM9) UNKNOWN (PROTEIN FOR MGC:8251).	(Q96BN2) Similar to RIKEN cDNA 2900026B15 gene.	(Q9NX85) CDNA FLJ20378 FIS, CLONE KAIA0536.
.64	HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64
	657		72	73	74	75	859	77
	1049830		793786	842802	625923	1306706	598022	520329
	HBOEG11		HBOEG69	HBXFL29	HCACU58	HCACV51	HCACV51	нсет089

HCE2F54	634016	78	HMMER	PFAM: Histone-like	PF00808	19	898	1005
			2.1.1	transcription factor				
				(CBF/NF-Y) and archaeal				
		;		histone				
			WUblastx	(AAH07642) Unknown	AAH07642	85%	298	1122
			.64	(protein for				
				IMAGE:3534358) (Fra				
HCEFB80	1143407	79	WUblastx	(Q96FR3) Unknown	Q96FR3	100%	1785	1979
			.64	(protein for MGC:18083).				
HCEFB80	1046853	659	WUblastx	(Q96FR3) Unknown	Q96FR3	100%	1777	1971
			.64	(protein for MGC:18083).				
HCEGR33	425212	08	WUblastx	(O9H743) CDNA:	Q9H743	51%	1002	1079
		<u>'</u>	.64	FLJ21394 FIS. CLONE	,	42%	1379	1492
				COL03536.		28%	206	993
HCEMP62	684780	81	WUblastx	(O8WZ37) Hypothetical	Q8WZ37	75%	484	897
			.64	43.7 kDa protein.	,	78%	88	459
				4		41%	-	183
-						94%	870	926
HCEWE17	941941	83	WUblastx	(O9H310) RH TYPE B	09Н310	%56	6	341
			49	GLYCOPROTEIN.	,	100%	425	463
					-	95%	444	999
HCEWE17	893535	199	WUblastx	(09H310) RH TYPE B	Q9Н310	%87	467	580
			49.	GLYCOPROTEIN.	,	75%	569	730
						100%	929	714
						100%	3	482
HCEWE17	460407	799	WUblastx	(Q9H310) RH TYPE B	Q9H310	%96	7	105
			.64	GLYCOPROTEIN.				
HCEWE20	543370	84	WUblastx	(Q9P1J1) PRO1546.	Q9P1J1	%9L	501	551
			.64			79%	601	717
HCFOM18	553582	88	WUblastx	(Q9H728) CDNA:	Q9H728	%09	621	490

		2188	2811	425	620		481		751					409	908	-		:	637				683				115	69	
		3069	3371	622	180		224		107					161	408	_			8				21			****	99	<u> </u>	
		%66	64%	24%	91%		32		%86					100%	%66				100%				100%		<u>.,,</u>		94%	91%	
		AAL76113			AAH00499		PF00047		060487					O60487					DVL2_HUMAN				DVL2_HUMAN				DVL2_HUMAN		
FLJ21463 FIS, CLONE	COL04765.	(AAL76113) Androgen-	induced basic leucine	zipper.	(AAH00499) Jumping	translocation breakpoint.	PFAM: Immunoglobulin	domain	(060487) EPITHELIAL	V-LIKE ANTIGEN	PRECURSOR	(EPITHELIAL V-LIKE	ANTIG	(060487) EPITHELIAL	V-LIKE ANTIGEN	PRECURSOR	(EPITHELIAL V-LIKE	ANTIG	(014641) SEGMENT	POLARITY PROTEIN	DISHEVELLED	HOMOLOG DVL-2	(014641) SEGMENT	POLARITY PROTEIN	DISHEVELLED	HOMOLOG DVL-2	(014641) SEGMENT	POLARITY PROTEIN	DISHEVELLED
.64		WUblastx	.64		WUblastx	.64	HMMER	2.1.1	WUblastx	.64				WUblastx	.64				WUblastx	.64			WUblastx	.64			WUblastx	.64	
		68			663		95							999					96				999				299		
		1352270			658672		637547							589445					1134974				1045182				1045183		
		HCHNF25			HCHNF25		HCNSM70							HCNSM70					HCOOS80				HCOOS80				HCOOS80		

1 1		HOMOLOG DVL-2				
98 WUblastx .64		hypothetical protein DKFZp564J157.1 - human (fragment)	pir T34520 T34520	97%	21	524
99 WUblastx (.64 F		(Q96MM0) CDNA FLJ32172 fis, clone PLACE6000555	О96МІМ0	79%	1043	972
100 WUblastx ((64 H		(Q9H3W5) HYPOTHETICAL 79.4 KDA PROTEIN.	Q9H3W5	100%	11	316
668 HMMER PF 2.1.1 Re	F 78	PFAM: Leucine Rich Repeat	PF00560	92.1	1190	1261
14		(Q9H3W5) HYPOTHETICAL 79.4 KDA PROTEIN.	Q9H3W5	100%	770	2893
102 WUblastx (Q9	6	(Q92WW6) Putative	Q92WW6	41%	264	335
. 64	sen	sensor histidine kinase protein.	,	45% 38%	166 301	231
669 HMMER PF.		PFAM: Domain found in bacterial signal proteins	PF00672	40.4	442	651
_	_	sensor histidine kinase	pir A87396 A87396	36%	379	915
		[imported] - Caulobacter crescentus		31%	268	363
670 HMMER PF		PFAM: Domain found in bacterial signal proteins	PF00672	41.6	350	559
+	+	sensor histidine kinase	pir A87396 A87396	36%	287	823
		[imported] - Caulobacter crescentus		31%	176	271
103 WUblastx (O	+	(060448) NEURONAL	060448	43%	2724	2371
.64	-	THREAD PROTEIN		75%	2373	2326

		AD7C-NTP.		63%	2776	2447
		- "		%59	2758	2579
≥	WUblastx	(Q9NX85) CDNA	Q9NX85	77%	538	419
.64		FLJ20378 FIS, CLONE	,	%95	710	699
		KAIA0536.		63%	708	532
M	WUblastx	(Q9NWD1)	Q9NWD1	94%	2	175
64		HYPOTHETICAL 61.6 KDA PROTEIN.		73%	1103	1303
M	olastx	(Q9UPI3)	Q9UPI3	100%	92	939
64	.64	HYPOTHETICAL 57.2				
		KDA PROTEIN.				
WUE	WUblastx	(Q9BTK4) UNKNOWN	Q9BTK4	100%	669	988
.64		(PROTEIN FOR MGC 4663)				
HMIN	HMMER	PFAM: Cytochrome P450	PF00067	21.7	145	282
2.1.1						
WUbl	astx	(Q9BTK4) UNKNOWN	Q9BTK4	100%	069	881
.64		(PROTEIN FOR				
		MGC:4003).				
WUblastx .64	astx	(Q9Y5Y5) PEROXISOMAL	Q9Y5Y5	81%	277	1284
		BIOGENESIS FACTOR				
HMI	1ER	PFAM: Sodium/calcium	PF01699	121.4	178	615
2.1.1	2.1.1	exchanger protein				
WUE	WUblastx	(Q9HC58)	09НС58	%06	10	657
.64		SODIUM/CALCIUM				
		EXCHANGER NCKX3.				
HIM	HMMER	PFAM: Sodium/calcium	PF01699	22.9	187	273
2.1.1		exchanger protein				

	_												_											
3891	1168	1231	592	1378		984		1051	603	461	1928				1859			1999	264	322	1551	1541	2407	2676
3700	761	1019	2	29		37		599	103	51	06				21			1532	169	182	1456	186	2369	2377
28%	%56	20%	%66	%66		95%		%56	%68	126.8	100%			_	%66			100%	65%	44%	21%	93%	53%	26%
Q8WVP7				Q9UBJ4		088407		088407		PF01027	Q9BRE2	,			Q9BRE2			Q9H2V9	,				Q9H387	
(Q8WVP7) Hypothetical	55.1 kDa protein.			(Q9UBJ4)	I KANSPOSASE-LIKE PROTEIN.	(O88407) NEURAL MEMBRANE PROTEIN	35.	(088407) NEURAL	MEMBRANE PROTEIN 35.	PFAM: Uncharacterized protein family	(Q9BRE2)	HYPOTHETICAL 68.4	KDA PROTEIN	(FRAGMENT).	(Q9BRE2)	HYPOTHETICAL 68.4	KDA PROTEIN	(09H2V9) CDA08.					(Q9H387) PRO2550.	
WUblastx	.64			WUblastx	.04	WUblastx .64		WUblastx	.64	HMMER	WUblastx	.64			WUblastx	.64		WUblastx	.64				WUblastx	.64
111				112		114		674		675	115				9/9			219					116	
547772				662269		1352360		862851		590733	1160316				727200			290988					740748	
HDHMA72				HDLAC10		HDPBI32		HDPBI32		HDPBI32	HDPBQ71	,			HDPBQ71			HDPBQ71	,				HDPCJ91	

1521	1809	834	840 1808		499	620	006	804	1086		562	1123		
199	76	199	76		146	877	895	610	139		305	218		
627.5	%66	324	%66 %66		%86	97%	16%	53.2	%66		26.9	%66		
PF01532	09Н886	PF01532	988H6Ò		Q9BXR1			PF00047	Q9BXR1		PF00047	Q9HD18		
PFAM: Glycosyl hydrolase family 47	(Q9H886) CDNA FLJ13869 FIS, CLONE THYRO1001287, WEAKLY SIMILAR TO MAN	PFAM: Glycosyl hydrolase family 47	(Q9H886) CDNA FLJ13869 FIS, CLONE THYRO1001287.	WEAKLY SIMILAR TO MAN	(Q9BXR1)	COSTIMULATORY MOI ECITIE	MODEL OF THE	PFAM: Immunoglobulin domain	(Q9BXR1)	COSTIMULATORY MOLECULE.	PFAM: Immunoglobulin domain	(Q9HD18)	TRANSMEMBRANE	LIGAND (B7-RELATED PROTEIN-
HMMER 2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx .64		WUblastx	.64		HMMER 2.1.1	WUblastx	4o	HMMER 2.1.1	WUblastx	.64	
118		829			119			629			089			
837699	·	604114			898208			1056541			997408			
HDPCY37		HDPCY37			HDPFB02			HDPFB02			HDPFB02			

AND PALATE	21	70	10/0/	AAU0/03/	(AADV/63/) UIMIOWII	w Colastx	000	882028	HDFMM88
CONTRACT	16	63	760/	A A LIO 7027	(A ATTAGON TELEMENT	11/1 11/1004.	607	020200	001/11/100
AND PALATE					TRANSPORTING ATPASE ID (EC			4	
Colored Colo					PHOSPHOLIPID-	.64			
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (PROTEIN FOR INAGE 158 1093 158% 1093 158% 1093 158% 1093 158% 1093 158% 1093 158% 1095 1095 1095 1095 1095 1095 1095 1095	172	2	73%	ATID_MOUSE	(P98199) POTENTIAL	WUblastx	682	902299	HDPMM88
COUNTY C					similar to PRO				
CONTROLLED CON					BRACE2007138, weakly				
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (Q14288) HYPOTHETICAL PROTEIN (PRAGMENT). PROTEIN (Q9BSQ8) UNKNOWN (Q9BSQ8)	365	8	%9 <i>L</i>		FLJ30324 fis, clone	.64			
CONTROLLED CON	403	356	%05	796NQ7	(Q96NQ7) CDNA	WUblastx	681	906121	HDPMM88
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL HYPOTHETICAL PROTEIN (PRAGMENT). (Q9BSQ8) UNKNOWN (PRAGMENT). PFAM: E1-E2 ATPase (P98198) POTENTIAL PHOSPHOLIPID- TRANSPORTING					ATPASE ID (EC				
(ADDOLE) LLI LLI COURT FOUR 97 RAND PALATE 100% 97 TRANSMEMBRANE PROTEIN 1. 614 PROTEIN 1. 47% 614 (Q14288) 47% 614 HYPOTHETICAL 88% 1297 PROTEIN 28% 1767 PROTEIN 39% 1093 RAGMENT). 35% 1275 (Q9BSQ8) UNKNOWN Q9BSQ8 94% 105 (PROTEIN FOR 36% 158 IMAGE:3510191) 93% 19 (FRAGMENT). PFAM: E1-E2 ATPase PF00122 31 475 PFAM: E1-E2 ATPase PFO0122 31 475 PHOSPHOLIPID- 32% 2917					TRANSPORTING				
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) (Q1	2991	2917	32%		PHOSPHOLIPID-	.64			
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (Q9BSQ8) UNKNOWN (PROTEIN FOR IMAGE:3510191) (FRAGMENT). PFAM: E1-E2 ATPase (D00000000000000000000000000000000000	2907	106	%89	ATID_HUMAN	(P98198) POTENTIAL	WUblastx			
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). Q04288 47% 614 48% 909 1297 48% 1093 35% 1275 2282 (Q9BSQ8) UNKNOWN Q9BSQ8 1MAGE:3510191) FRAGMENT). GAM. E1 E2 A TBood AND PALATE 100% 97 914 915 915 915 915 915 915 915 915 915 915	 F	C F	10	11.00122	FIMIN EI-EZ MIFASE	2.1.1	071	417174	
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). (Q9BSQ8) UNKNOWN Q9BSQ8 IMAGE:3510191) FRANSMEMBRANE PROTEIN (Q9BSQ8) UNKNOWN Q9BSQ8 IMAGE:3510191) FRAGMENT). (A14288 FRAGMENT) FRAGMENT	5/12	371	21	DE00122	DEAM. E1 E2 ATDees	TIMARED	106	077774	The And Aloo
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN PORTION (Q9BSQ8) UNKNOWN	CCI	61	93%		IMAGE:3310191) (FRAGMENT).				
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). (Q9BSQ8) UNKNOWN (Q9BSQ8) (Q9BSQ8)	017	100	0/00		(FNOIEM FOR	5.			
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). (Q9BSO8) UNKNOWN PROTEIN (O9BSO8) UNKNOWN PROTEIN (O9BSO8) UNKNOWN PROTEIN (FRAGMENT). (1007) (100	718	150	360/	972117	(DDOTEIN FOD	64	<u></u>	· · · · · · · · · · · · · · · · · · ·	
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). (FRAGMENT). (COMMENT). (A14288 (A14	650	105	94%	09BSO8	(09BSO8) UNKNOWN	WUblastx	125	704487	HDPJF37
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). AND PALATE 100% 97 614 614 614 618 88% 1297 88% 11093 35% 11093	2082	2282	27%						
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT). (Q14288) (Q148	1090	1275	35%					_	
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN (FRAGMENT).	068	1093	39%						
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL PROTEIN PROT	1537	1767	28%		(FRAGMENT).				
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) HYPOTHETICAL 88% 1297 1100% 97 614 614 1100% 97	1007	606	48%		PROTEIN				
AND PALATE TRANSMEMBRANE PROTEIN 1. (Q14288) (Q14288) (Q14288) (Q14288)	1271	1297	%88		HYPOTHETICAL	.64			
AND PALATE TRANSMEMBRANE PROTEIN 1.	216	614	47%	Q14288	(Q14288)	WUblastx	123	823355	HDPGP94
AND PALATE TRANSMEMBRANE					PROTEIN 1.				
AND PALATE 100% 97 7					TRANSMEMBRANE				
(0,000) CECT I LII	762	97	100%		AND PALATE	.64			
(CO66005) CLEET LTD CO66005 100% 3	29	n	100%	200960	(096005) CLEFT LIP	WUblastx	120	288697	HDPFF39

			.64	(protein for		 %69	298	62
HDPMM88	874074	684	WUblastx	(P98198) POTENTIAL	ATID HUMAN	65%	1023	
			.64	PHOSPHOLIPID-	-			
				TRANSPORTING			<u> </u>	_
!				ATPASE ID (EC				
HDPNC61	637585	127	WUblastx	(Q8WY51) HC6.	Q8WY51	52%	654	827
			.64			64%	37	78
HDPND46	637586	128	WUblastx	(Q9BR26) DJ257E24.3	Q9BR26	81%	12	1466
			.64	(NOVEL PROTEIN)	,			
				(FRAGMENT).				
HDP0E32	897276	129	WUblastx	(Q9BW48) MY047	Q9BW48	%86	64	345
			.64	PROTEIN.				
НОРОН06	683371	130	HMMER	PFAM: Uncharacterized	PF01554	8.06	255	969
			2.1.1	membrane protein family	!			
			WUblastx	l .	Q96FL8	%66	18	226
			.64	61.9 kDa protein.				
HDPOZ56	1352319	131	WUblastx		BAB84923	100%	28	1791
			.64	protein (Fragment).				
HDPOZ56	815653	289	HMMER		PF01593	431.1	307	1614
			2.1.1	amine oxidase				
			WUblastx	(BAB84923) FLJ00168	BAB84923	%66	40	1800
			.64	protein (Fragment).				
HDPOZ56	743479	889	HMMER	PFAM: Flavin containing	PF01593	185.2	200	946
	!	!	2.1.1	amine oxidase				
			WUblastx	(BAB84923) FLJ00168	BAB84923	%86	197	958
			.64	protein (Fragment).		%66	952	1647
						100%	2	202
HDPSP54	744440	132	WUblastx	(BAB85063) CDNA	BAB85063	%66	7	307
			.64	FLJ23790 fis, clone				

	833	1126	1599	1733 290	1005	1440	294 473 294 1610 521 1487 1607 294 1861 1544 1478
	937	1013 102	55	261	844	40	235 288 244 288 456 1215 1389 238 1607 798 1317
	%16	97%	%96	%69 %08	38.9	100%	95% 38% 58% 40% 29% 31% 42% 27% 42%
	Q9BU29	BAB11849	Q9BVK2	Q8VHE7	PF00047	Q9Y286	BAB55096
HEP21466.	(Q9BU29) UNKNOWN (PROTEIN FOR IMAGE:3954899) (FRAGMENT).	(BAB11849) MOP-2.	(Q9BVK2) UNKNOWN (PROTEIN FOR MGC:2840).	(Q8VHE7) Hypothetical 67.5 kDa protein.	PFAM: Immunoglobulin domain	(Q9Y286) QA79 MEMBRANE PROTEIN, ALLELIC VARIANT AIRM-1B PRECURSOR.	(BAB55096) CDNA FLJ14508 fis, clone NT2RM1000421, w
	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx .64
	133	134	135	136	137		138
	692917	744824	684120	866433	812737		796865
	HDPTD15	HDPTK41	HDPUG50	НDРUH26	HDPUW68		НДРУН60

1903	1906	2032	2077	1903	1598	294	1344		1991	1332	2097	200	1647	397		2450		199	714	155	2487	857	1091
1613	1607	1658	1580	1628	1200	238	913		1344	1096	1924	9	13	2		45		35	619	27	205	432	3
30%	25%	27%	%98	76%	35%	42%	30.2		52%	27%	%98	30%	73%	84%		%66		%16	%89	%89	%66	77.2	100%
							PF00501		Q9BTY5					Q9BTY5		AAH25255	!	AAH25255		Q9H747		PF00854	Q9P2X9
							PFAM: AMP-binding	enzyme	(Q9BTY5) UNKNOWN	(PROTEIN FOR	MGC:4365).			(Q9BTYS) UNKNOWN	MGC:4365).	(AAH25255) Similar to	hypothetical protein FLJ21347	(AAH25255) Similar to	hypothetical protein FLJ21347	(Q9H747) CDNA:	FLJ21347 FIS, CLONE COL02724.	PFAM: POT family	(Q9P2X9) PEPTIDE TRANSPORTER 3.
		-					HMMER	2.1.1	WUblastx	.64				WUblastx 64		WUblastx	.64	WUblastx	.64	WUblastx	.64	HMMER 2.1.1	WUblastx .64
							139							069		140		169		692		141	
							1036997			_				896530		992925		887914		905983		630354	
							HDPVW11							HDPVW11		HDPWN93		HDPWN93		HDPWN93		HDPWU34	

HUCHUUS	1309175	142	WUblastx	(AAH25621)	AAH25621	%98	520	1263
			.64	Hypothetical 137.4 kDa				
				protein (Fragment			-	
нронр03	834692	694	HMMER	PFAM: Cyclic nucleotide-	PF00027	44.3	602	870
			W/I lbloctv	Oniding dollain	1695601	0/0/	505	12/8
			w Oblasta	(AAH23021)	AAU23021	0/1/0	COC	0471
			.64	Hypothetical 137.4 kDa protein (Fragment		·		
HDTBD53	972757	143	WUblastx	(Q9BTV4) UNKNOWN	Q9BTV4	100%	183	1382
			.64	(PROTEIN FOR	,			
!				MGC:3222).				
HDTBD53	906342	695	WUblastx	(Q9BTV4) UNKNOWN	Q9BTV4	%66	187	1386
			.64	(PROTEIN FOR			· .	
				MGC:3222).				
HDTBP04	1307742	144	WUblastx	(Q9D5J3)	Q9D513	38%	70	720
			.64	4930432K09RIK				
				PROTEIN.				
HDTBP04	543618	969	WUblastx	(090513)	Q9D513	38%	59	718
			.64	4930432K09RIK				
				PROTEIN.				
Н DТDQ23	1306984	145	WUblastx	calcium-binding protein	pir S04970 S04970	100%	1611	1709
			.	(clone pMP41) - mouse				
				(fragment)				
Н DТDQ23	879009	269	WUblastx	calcium-binding protein	pir S04970 S04970	100%	1623	1721
		. <u> </u>	.64	(clone pMP41) - mouse				
		000		(fragment)		2007	000	
HDTDQ23	751707	869	WUblastx	calcium-binding protein	pir S04970 S04970	100%	1623	1721
		·	†	(fragment)				
HDTFE17	1043391	148	WUblastx	(Q9UJU8) JM24	80rn60	100%	14	118

955 1 343		337	337 116 457 33	337 116 116 457 33 463	337 116 116 457 33 463 819 819 352	337 116 457 33 463 819 352 343	337 116 457 33 463 819 819 352 343 1119 1	337 116 457 33 463 819 352 352 343 1119 1 1351 1	337 116 116 457 33 463 463 819 352 352 352 353 1119 1119 1351 1351
10001	100% 45% 72%		86.4	86.4 100% 97% 50.9	86.4 100% 97% 50.9 100% 82%	86.4 100% 97% 50.9 100% 82% 82%	100% 97% 50.9 100% 82% 82% 64% 72%	100% 97% 50.9 100% 82% 82% 72% 100%	86.4 100% 97% 50.9 82% 82% 72% 100%
	-	0							
1490	1490	21.17/	V 1 UZ	1161	1161 5DV4	DV4	DV4	DV4 DV4 1728 3S33	1161 1161 1DV4 1728 3S33 WX31
Q8 W 1 U2 PF01490	PF01490	Q8WYU2		PF01161	PF01161 Q96DV4	PF01161 Q96DV4 Q96DV4	PF01161 Q96DV4 Q96DV4	PF01161 Q96DV4 Q9H728 Q9BS33	PF01161 Q96DV4 Q9H728 Q9BS33 Q8WX31
omencal 	44.0 kDa protein.	nbrane oorter othetical	44.0 kDa protein.	anolamine	- 			44.0 kDa protein. PFAM: Phosphatidylethanolamine-binding protein (Q96DV4) Similar to RIKEN cDNA 4733401F03 gene. (Q96DV4) Similar to RIKEN cDNA 4733401F03 gene. (Q96DV4) Similar to RIKEN cDNA ELI21463 FIS, CLONE COL04765. (Q9BS33) SIMILAR TO HYPOTHETICAL PROTEIN FLJ11218.	44.0 kDa protein. PFAM: Phosphatidylethanolamine-binding protein (Q96DV4) Similar to RIKEN cDNA 4733401F03 gene. (Q96DV4) Similar to RIKEN cDNA 4733401F03 gene. (Q9H728) CDNA: FLJ21463 FIS, CLONE COL04765. (Q9BS33) SIMILAR TO HYPOTHETICAL PROTEIN FLJ11218. (Q8WX31) BA382H24.3 (multiple PDZ domain protein) (Fragment).
MER	 	olastx		L		L L L			
		WUI							
707	1	117 703		264 150					
8/44//		892317		839264	83926	839264	839264 834697 1011485	839264 834697 101148	839264 834697 1011485 722217 396139
HD1FE1/		HDTFE17		F10	L10	T10	TT10	TT10 T10 AKS0 Y70	HDTIT10 HDTIT10 HE2DY70 HE2FV03

				GROUP (NONHISTONE CHROMOSOMAL) PROT				
НЕ2РD49	638617	157	WUblastx .64	(Q9BSR6) SIMILAR TO RIKEN CDNA 2410018G23 GENE.	Q9BSR6	100%	403	849
HE8DS15	847060	160	WUblastx .64	(Q9WVT0) SEVEN TRANSMEMBRANE RECEPTOR.	Q9WVT0	80% 24% 87%	1 48 269	270 146 985
HE8MH91	589450	161	WUblastx .64	(Q9H8Z4) CDNA FLJ13121 FIS, CLONE NT2RP3002687.	О9Н8Z4	%86	6	410
НЕ8QV67	1050076	162	WUblastx .64	(BAB55430) CDNA FLJ14978 fis, clone VESEN1000122.	BAB55430	100% 31% 100% 96% 96%	321 487 1 1403 577	425 600 201 1684 729
HE8QV67	1050077	707	WUblastx .64	(BAB55430) CDNA FLJ14978 fis, clone VESEN1000122.	BAB55430	100% 86% 30% 30% 99%	1500 3 109 1366 334	1108 1988 206 246 1455
HE9BK23	675382	163	HMMER 2.1.1	PFAM: Fibrinogen beta and gamma chains, C- terminal globular domain	PF00147	77.2	762	959
			WUblastx .64	(Q9Y5C1) ANGIOPOIETIN 5.	Q9Y5C1	100%	958	1419 959
HE9DG49	1299935	165	WUblastx .64	(Q9NYL4) FK506 BINDING PROTEIN	Q9NYL4	100%	70	672

	492	672	-352	679 674	1151	966	497	2087	858 1076 332 1015 864 703
	211	70	-71	578 78	129	142	129	1995	691 1020 210 833 784 332
	91	100%	91	100% 86%	%56	%66	93%	40%	57% 89% 75% 78% 33% 55%
	PF00254	Q9NYL4	PF00254	Q9NYL4	CAC41349	CAC41349	CAC41349	09NV86	pir S72481 S72481
PRECURSOR.	PFAM: FKBP-type peptidyl-prolyl cis-trans isomerases	(Q9NYL4) FK506 BINDING PROTEIN PRECURSOR.	PFAM: FKBP-type peptidyl-prolyl cis-trans isomerases	(Q9NYL4) FK506 BINDING PROTEIN PRECURSOR.	(CAC41349) Alpha2-glucosyltransferase.	(CAC41349) Alpha2-glucosyltransferase.	(CAC41349) Alpha2-glucosyltransferase.	(Q9NV86) CDNA FLJ10873 FIS, CLONE NT2RP4001730, WEAKLY SIMILAR TO UDP	probable transposase - human transposon MER37
	HMMER 2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64
	708		709		168	710	711	169	170
	658678		382000		1352337	838598	834400	886167	561524
	HE9DG49		HE9DG49		HE90W20	HE90W20	HE90W20	HE9RM63	HEAAR07

HEBCM63	484643	173	olastx	(Q9BYH1) SEZ6L.	Q9ВҮН1	%16	12	449
HEBEJ18	701802	174	.04 WUblastx	(AAH00573) HSPC163	AAH00573	100%	51	467
HEEAG23	684254	175	HMMER	PFAM: emp24/gp25L/p24	PF01105	36.2	63	185
			WUblastx	(AAH23041) Similar to	AAH23041	100%	114	185
			.64	RIKEN cDNA 2400003B06 gene.		%66	406	780
HEEAJ02	633657	176	WUblastx	(Q9BW86)	Q9BW86	%08	54	761
			.64	PHOSPHATIDYLETHA NOLAMINE N-				
		s		METHYLTRANSFERAS E.				
HEEAQ11	777843	177	HMMER 2.1.1	PFAM: Cystatin domain	PF00031	39.7	360	638
			WUblastx	(Q9H4G1) BA218C14.1	Q9H4G1	100%	213	653
			.64	(NOVEL CYSTATIN				
				FAMILY MEMBEK).				
HEEBI05	1307611	178	WUblastx .64	(Q9N7S5) PROBABLE PROTEOPHOSPHOGLY	Q9N7S5	32%	252	635
				CAN (FRAGMENT).				
HEEBI05	1047700	712	WUblastx	(Q9N7S5) PROBABLE	Q9N7S5	32%	332	715
		.—_	.64	PROTEOPHOSPHOGLY			_	
				CAN (FRAGMENT).				
HEGAH43	532596	179	WUblastx	(Q9H1M5) BA530N10.1	Q9H1M5	100%	29	361
			.64	(NOVEL PROTEIN).				
HEGAN94	885637	180	WUblastx	colipase precursor,	pir A46717 A46717	36%	148	393
			.64	pancreatic - dog				
HEGAN94	769649	713	HMMER	PFAM: Colipase	PF01114	24	229	405

2.1.1
x colipase precursor, pancreatic - dog
WUblastx (Q9H056) .64 HYPOTHETICAL 12.5
HMMER PFAM: DHHC zinc finger 2.1.1 domain
i
FLJ 10479 F1S, CLOINE NT2RP2000120 (DC1) HVPOTHFTYCAL 39
HMMER PFAM: DHHC zinc finger
_1
FLJ104/9 F1S, CLOINE NT7RP2000120 (DC1)
WUblastx (Q9N083) UNNAMED
PFAM: DHHC zinc finger domain
WUblastx hypothetical protein .64 DKFZp761E1347.1
HMMER PFAM: DHHC zinc finger

DKFZp761E1347.1

471	744	745	386	841	545 582	795	647	1022		1022		256	46	253	797	722	699	
10	385	398	18	999	405 541	646	3	3		3		101	2	53	237	672		
%06	63%	83%	100%	%96	95%	%86	%66	%66		%66		%86	100%	%56	%88	94%	%69	
	Q8VDR1	Q8VDR1	9Нd96Ò	6XMM8D		Q9NXH2	,	AAH25323		AAH25323		AAH25323		Q9QZE9		Q9Y6F6		
human (fragment)	(Q8VDR1) Similar to RIKEN cDNA 2310044D20 gene.	(Q8VDR1) Similar to RIKEN cDNA 2310044D20 gene.	(Q96РН6) ESC42.	(6XMM89)	Selenoprotein SelM.	(Q9NXH2) CDNA	FLJ20254 FIS, CLONE COLF6926.	(AAH25323) Similar to	hypothetical protein FLJ21240	(AAH25323) Similar to	hypothetical protein FLJ21240	(AAH25323) Similar to	hypothetical protein FLJ21240	(Q9QZE9) TM6P1.		(Q9Y6F6) JAW1-	RELATED PROTEIN	MRVI1A LONG ISOFORM.
	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx		WUblastx	.64	WUblastx	.64	WUblastx	.64	WUblastx	.64	WUblastx	.64	WUblastx	.64	
	185	717	186	190		191		193		719		720		194		195		
	741647	419870	596830	526013		609827		1177512		1046327		1046328		847073		490697		
	HEMAM41	HEMAM41	HEPAA46	HESAJ10		HETAB45		HETLM70	,	HETLM70		HETLM70		HFABG18		HFAMB72		

365 1042	35 1102	568 657	249 410	833 919		423 458	987 1145	1038 1196	884 970	74 241	474 509		1230 1397	1444 1533	1390 1434	1471 1533	11 265	253 564	161 1831				741 890
130.8	95%	100%	92%	8 %66			6 %86			%86	91%		54% 12	42% 14	66% 13	50%	%68	100%	100%				46.3
PF01762	Q9C0J1	075525	pir 178556 178556	6XMM89				6XMM8D				Q9HAD8			_		tr_vs 095742-	01 095742	095970				PF01463
PFAM: Galactosyltransferase	(Q9C0JI) BETA-1,3-N-ACETYLGLUCOSAMIN YLTRANSFERASE BGN-T4.	(075525) T-STAR.	membrane glycoprotein M6 - mouse	(Q8WWX9)	Selenoprotein SelM.			(Q8WWX9)	Selenoprotein SelM.			(Q9HAD8) CDNA	FLJ11786 FIS, CLONE	HEMBA1006036.			ISOFORM OAT1.2 OF	095742	(095970) LEUCINE-	RICH GLIOMA-	INACTIVATED	PROTEIN PRECURSOR.	PFAM: Leucine rich
HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx	.64			WUblastx	.64			WUblastx	.64				WUblastx	.64	WUblastx	.64			HMMER
197		200	201	202				721				203					204		208				722
579993		560639	513669	1043350				802906				889515					634743		1309793				835390
Н FCCQ50		HFFAL36	HFGAD82	HFIIZ70			-	HFIIZ70				HFKET18			· .		HFKFG02		HFPCX09				HFPCX09

	225 1895		161 298	169 1830				450 680		20 802			168 1574		93 1649						133 714					
	%66		%98	94%			%95	%99		%88			6.697		%66		-	-	 		100%	100%	100%	100%	100%	100%
	029570		095970				Q96NR6			096B80			PF00065		ACHG_MOUSE						Q9BX93	Q9BX93	Q9BX93	Q9BX93 Q9BX93	Q9BX93 Q9BX93	Q9BX93 Q9BX93
repeat C-terminal domain	(095970) LEUCINE- RICH GLIOMA-	INACTIVATED PROTEIN PRECURSOR.	(095970) LEUCINE-	RICH GLIOMA-	INACTIVATED	PROTEIN PRECURSOR.	(Q96NR6) CDNA	FLJ30278 fis, clone	BRACE2002755.	(Q96B80) Similar to	RIKEN cDNA	0610040E02 gene.	PFAM: Neurotransmitter-	gated ion-channel	(P04760)	ACETYLCHOLINE	RECEPTOR PROTEIN,	GAMMA CHAIN	PRECUR	TITY OF COVOCO	(CARAS) GROOF AIII	(QSBASS) GROOF AIII SECRETED	(QYBAY3) GROOF AIII SECRETED PHOSPHOLIPASE A2.	SECRETED PHOSPHOLIPASE A2. (Q9BX93) GROUP XIII	SECRETED PHOSPHOLIPASE A2. (Q9BX93) GROUP XIII SECRETED	SECRETED PHOSPHOLIPASE A2. (Q9BX93) GROUP XIII SECRETED PHOSPHOLIPASE A2.
	WUblastx .64		WUblastx				WUblastx			WUblastx			HMMER			.64						.64	.64	.64 WUblastx	.64 WUblastx .64	.64 WUblastx .64
			723				209			211			212							214				725	725	725
			598723				526635		-	735139	·		92669							1300736				565076	565076	565076
			HFPCX09				HFPCX36			HFTCU19			HFTDL56							HFVAB79				HFVAB79	HFVAB79	HFVAB79

1042	292 525	1015	768 815	140 1147	1494 439	1403	1257	1505	537	950	728 580	601
1164	492 920	5	812 928	72 134	1387	482 723	736	1251	223	12	540 245	17
28%	34% 36%	81%	%0 <i>L</i> %98	%96 %96	50%	62%	65%	81%	27%	71%	85% 81%	%86
096Н6О	062658	О9Н5Н7	Q9P147	AAH06833	pir T28058 T28058		Q9V3N6			9N8N6	AAH06738	О9H763
(Q9H960) CDNA FLJ12988 FIS, CLONE NT2RP3000080.	(O62658) LINE-1 ELEMENT ORF2.	(Q9H5H7) CDNA: FLJ23425 FIS, CLONE HEP22862.	(Q9P147) PRO2822.	(AAH06833) Similar to DKFZP586F1524 protein.	hypothetical protein ZK858.6 - Caenorhabditis	elegans	(Q9V3N6) BG:DS007071	PROTEIN.		(Q9V3N6) BG:DS00797.1 PROTEIN.	(AAH06738) Hypothetical 47.5 kDa protein.	(Q9H763) CDNA: FLJ21269 FIS, CLONE COL01745.
WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64		WUblastx 64	<u>.</u>		WUblastx .64	WUblastx .64	WUblastx .64
223	224	225	526	227	229		727			728	231	232
609826	505207	069859	634161	422794	837220		838602			899864	838603	1003028
НҒХНК73	HFXKJ03	HFXKT05	HFXKY27	HGBFO79	HGBIB74		HGBIB74			HGBIB74	HHAAF20	ННВСS39

883427	729	WUblastx	(Q9H763) CDNA:	69H763	%86	63	647
		.64	FLJ21269 FIS, CLONE				
			COL01745.		! ! !		:
638231	233	WUblastx	(Q9BVD9) UNKNOWN	Q9BVD9	61%	1923	1870
		.64	(PROTEIN FOR		74%	2147	1923
			MGC:5149).				
941955	236	WUblastx	(Q96QU0) Calcium-	000960	%66	1741	2046
		.64	promoted Ras inactivator.				
906815	732	WUblastx		Q9HBS7	%99	731	088
		.64	HYPOTHETICAL 14.2		64%	592	735
			KDA PROTEIN.		:		
902458	733	WUblastx	(Q96QU0) Calcium-	00096D	%66	458	1891
		.64	promoted Ras inactivator.	!	%68	140	253
895682	734	WUblastx	(Q96QU0) Calcium-	000960	83%	316	477
		.64	promoted Ras inactivator.		100%	287	316
877639	239	WUblastx	(Q96BH1) Ring finger	096ВН1	%26	10	1230
		.64			100%	1185	1373
838217	241	WUblastx	_	09BQB6	%08	259	747
		.64	(PROTEIN FOR				
			MGC:11276) (PROTEIN				
			FOR IMAGE:3455200).				
897457	735	blastx.2	(BC000828) Unknown	gb AAH00828.1 AA	%08	267	755
			(protein for	H00828			
			IMAGE:3455200) [Homo				
			sapiens]				:
535730	736	WUblastx	(Q9BQB6) UNKNOWN	Q9BQB6	72%	326	424
		.64	(PROTEIN FOR		83%	217	339
			MGC:11276) (PROTEIN		100%	45	218
			FOR IMAGE:3455200).				
821330	242	WUblastx	(Q9LGZ9) GENOMIC	6Z976Ò	100%	746	898

198	998	867	998	867	998	867	998	867	998	867	998	867	998	298	998	198	998	867	998	198	998	298	998	198	998	198	998	867	998	867
745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745
100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
DNA, CHROMOSOME	3, BAC CLONE:F1D9.																													
.64																														
				_																								_		
								_					_													-				
				~																										

998	198	998	198	998	867	998	298	998	298	998	867	998	867	998	198	998	867	998	867	998	867	998	867	998	867	998	198	998	198	998
744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744
100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
																-							-							
															-					-										
		. -	_																											-

/98	998	867	998	298	998	298	998	198	998	867	198	867	998	298	998	198	998	298	998	198	998	298	998	867	998	867	998	867	998	867
745	744	745	744	745	744	745	744	745	744	745	745	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745	744	745
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100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	%56	%56	%68	%55	49%	100%	36.3
																					Q9D1N2	Q9CWA7	Q96AP7	PF00047
																					(Q9D1N2) 1110002J19RIK PROTEIN.	(Q9CWA7) 0610010F05RIK PROTEIN (FRAGMENT).	(Q96AP7) Hypothetical 41.2 kDa protein.	PFAM: Immunoglobulin
																					WUblastx .64	WUblastx .64	WUblastx .64	HMMER
																					243	244	245	737
																					905849	634521	865581	691402
																					ННҒЕС49	HHFFJ48	HHFGR93	HHFGR93

	1298	828	762				G 		789	-	* 12,00	4	101		L89	620	353	496	114	536			114	536			787	887
	819	130	1			- 6	760		268			81	196		622	531	439	633	7	378			7	378			107	774
	%86	%66	100%			è	0/66		%66			61%	%06		%98	%99	46%	46%	%46	%86			%46	%86			%65	52%
	Q96AP7		6X766D			Colland	(J9H/F4		O9H7P4	,		Q9H7P4			Q96NR6				Q96FV2				Q96FV2				Q9P1J1	
domain	(Q96AP7) Hypothetical	41.2 kDa protein.	(Q99LX9) SIMILAR TO	SINGLE-SIRAINDED-	DINA-BINDING	FROI EIIN.	(Q9H/P4) FLJUUU24	(FRAGMENT)	(09H7P4) FL J00024	PROTEIN	(FRAGMENT).	(Q9H7P4) FLJ00024	PROTEIN	(FRAGMENT).	(Q96NR6) CDNA	FLJ30278 fis, clone	BRACE2002755.		(Q96FV2) Unknown	(protein for	IMAGE:3945715)	(Fragment).	(Q96FV2) Unknown	(protein for	IMAGE:3945715)	(Fragment).	(Q9P1J1) PRO1546.	
2.1.1	WUblastx	.64	WUblastx	.0 .		1 11 11 11	W U DI ASTX	, 0.	WUblastx	.64		WUblastx	.64		WUblastx	.64			WUblastx	.64			WUblastx	.64			WUblastx	.64
			247		-	9,0	847		738			739			249				250				740				253	
			411470			1107401	117/491		1040264			1042456			520198				662329				383547				554613	
			HHFHR32		·	001001111	HHFO129		HHFOJ29			HHFOJ29			HHGB091		_		HHGCM76				HHGCM76		•		HHGDW43	

HHPGO40	1299927	255	WUblastx	(Q9HBW1) Brain tumor	Q9HBW1	74%	191	926
	-			associated protein	,	30%	338	928
				NAG14.				
HHPGO40	753270	741	HMMER	PFAM: Leucine Rich	PF00560	122	542	613
			2.1.1	Repeat				
			WUblastx	(Q9HBW1) Brain tumor	Q9HBW1	74%	191	<i>L</i> 96
			.64	associated protein		30%	338	876
				NAG14.				,
HHPGO40	696095	742	HMMER	PFAM: Leucine Rich	PF00560	77	548	619
			2.1.1	Repeat				
			WUblastx	(Q9HBW1) Brain tumor	Q9HBW1	71%	739	984
			.64	associated protein		31%	691	933
				NAG14.		74%	197	754
HILCF66	636025	258	WUblastx	(Q9CWZ1)	Q9CWZ1	100%	1435	1530
			.64	2400006A19RIK	-	%96	1243	1323
				PROTEIN.				
HJACG02	1307789	259	WUblastx	(Q9HD89) CYSTEINE-	68ДН6О	100%	99	389
			.64	RICH SECRETED		_		
				PROTEIN (C/EBP-				
	.—.			EPSILON REGULATED				
				MYEL				
HJACG02	509948	743	WUblastx	(Q9HD89) CYSTEINE-	68UH60	100%	47	370
			.64	RICH SECRETED		,		
				PROTEIN (C/EBP-				
				EPSILON REGULATED				
				MYEL				
HJACG30	895505	260	WUblastx	(Q9UM21) UDP-	Q9UM21	%96	291	389
			.64	GLCNAC:A-1,3-D-				
				MANNOSIDE B-1,4-N-				
				ACETYLGLUCOSAMIN				

				YLTRANS				
	774300	745	WUblastx 6.4	(Q9D399)	Q9D399	%08	220	297
			+	9330413B21MIN PROTEIN.				
	877643	261	WUblastx .64	(Q9Y3P8) SIT PROTEIN PRECURSOR.	Q9Y3P8	100%	36	623
HJBCY35	719729	262	WUblastx .64	hypothetical protein DKFZp586J0619.1 -	pir T08758 T08758	100%	-	1212
нлмвм38	545752	264	WUblastx .64	(Q9CS66) 5730496N17RIK PROTEIN (FRAGMENT).	99S260	83%	8	722
HJPAD75	651337	267	WUblastx .64	(Q9H5F8) CDNA: FLJ23476 FIS, CLONE HSI14935.	Q9H5F8	%86	8	232
	852573	747	WUblastx .64	(Q9VL06) CG5604 PROTEIN.	907A6Ò	54%	19	315
	824612	748	WUblastx .64	cut1 protein - fission yeast (Schizosaccharomyces pombe)	pir A35694 A35694	42%	7	201
HKAAE44	564406	269	WUblastx .64	(Q969S6) Unknown (protein for MGC:15961) (protein for MGC:14327).	986960	%98	113	520
НКААН36	1352332	270	WUblastx .64	(AAH08036) Kallikrein 5.	AAH08036	100%	128	1006
НКААН36	1352331	749	WUblastx .64	(AAH08036) Kallikrein 5.	AAH08036	71%	295	846
НКААН36	1352330	750	WUblastx .64	(AAH08036) Kallikrein 5.	AAH08036	100%	182	1060

348	1108	1132	686	1007	353 1065	099	681	802	541	794	533	266	766	1199	715
184 399	452	254	327	129	189	457	16	11	137	69	129	114	96	786	125
%06 100%	270.2	%76	270.2	100%	100%	56.1	95%	%66	45%	%66	45%	76.3	%28	86%	100%
AAH08036	PF00089	AAH08036	PF00089	AAH08036	AAH08036	PF01762	Q8WWR6	68Т96О		096ГВ9		PF00050	IAC2_BOVIN	Q96ВН2	
(AAH08036) Kallikrein 5.	PFAM: Trypsin	(AAH08036) Kallikrein 5.	PFAM: Trypsin	(AAH08036) Kallikrein 5.	(AAH08036) Kallikrein 5.	PFAM: Galactosyltransferase	(Q8WWR6) Beta 1,6- GlcNAc-transferase.	(Q96LB9) Peptidoglycan	recognition protein-I-alpha precursor.	(Q96LB9) Peptidoglycan	recognition protein-I-alpha precursor.	PFAM: Kazal-type serine protease inhibitor domain	(P01001) ACROSIN INHIBITORS IIA AND IIB (BUSI-II).	(Q96BH2) Hypothetical 34 4 kDa protein	
WUblastx .64	HMMER 2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx	.64	WUblastx	.64	HMMER 2.1.1	WUblastx .64	WUblastx 64	
751	752		753		754	271		273		755		274		275	
836040	838088		815661		590734	589945		862030		665424		554616		1352202	
НКААН36	НКААН36		НКААН36		НКААН36	HKAAK02		HKABZ65		HKABZ65		HKACB56		HKACD58	

HKACD58	552465	756	WUblastx	(O96BH2) Hypothetical	096BH2	%98	795	1208
			.64	34.4 kDa protein.	,	28%	43	183
,				•		%88	122	724
HKACM93	1352383	277	blastx.14	aqualysin (EC 3.4.21) I	pir A35742 A35742	40%	884	1039
				precursor - Thermus		41%	1097	1276
			,	aquaticus		30%	1274	1468
-						20%	746	823
						34%	548	029
						53%	425	469
						28%	2201	2236
HKACM93	907085	758	WUblastx	aqualysin (EC 3.4.21) I	pir A35742 A35742	42%	937	1071
			.64	precursor - Thermus		35%	521	616
1117 A CIVION	006150	350	11/1 11.1.	adaancas Door 1	SEPP TIMER	/000	0	200
HKACM95	061906	00/	W U DIASTX	(F80146)	SEFK_IHESK	39%	- 0 4	600
			.64	EXTRACELLULAR				
				SERINE PROTEINASE				-
				PRECURSOR (EC 3.4.				
HKAEL80	570865	278	WUblastx	(O60448) NEURONAL	060448	63%	682	935
			.64	THREAD PROTEIN		%89	934	666
				AD7C-NTP.		65%	862	1052
HKAEV06	1352263	279	WUblastx	(Q9NVA4) CDNA	Q9NVA4	%66	501	1814
			.64	FLJ10846 FIS, CLONE				
				NT2RP4001373.				
HKAEV06	638238	761	WUblastx	(Q9NVA4) CDNA	Q9NVA4	%96	367	459
			.64	FLJ10846 FIS, CLONE		100%	197	367
				NT2RP4001373.		%96	480	1541
HKAFK41	545018	280	WUblastx	(BAB55101) CDNA	BAB55101	91%	18	371
			.64	FLJ14515 fis, clone		% 09	130	537
				NT2RM1000800, w				
HKAFT66	946512	281	WUblastx	(Q9CPS2)	Q9CPS2	72%	29	61

WUblastx (Q9CPS2) .64 4933428103RIK PROTEIN. PROTEIN. WUblastx (Q9CPS2) WUblastx (Q9HBJ8) KIDNEY- .64 SPECIFIC MEMBRANE PROTEIN NX-17. WUblastx (Q9HBJ8) KIDNEY- SPECIFIC MEMBRANE PROTEIN NX-17. WUblastx (Q9HBJ8) CDNA WUblastx (Q9H919) CDNA	2		010%		
	A		0/1/0	274	828
	2	Q9CPS2	72%	29	61
	-		64%	61	231
 			83%	274	828
		Q9CPS2	%08	298	555
			84%	12	314
	NEY-	Q9HBJ8	%88	69	734
 	EMBRANE -				
		Q9HBJ8	100%	18	257
╂	NE	,	%08	239	685
_		Q9H919	73%	307	239
FLJ13078 FIS, CLONE	CONE		80%	128	84
NT2RP3002002	72.		63%	228	121
WUblastx (Q9H919) CDNA	NA	О9Н919	73%	314	246
FLJ13078 FIS, CLONE	, CLONE		24%	1056	206
NT2RP3002002	32.		%08	135	91
			63%	235	128
astx (Q8WWW1) Smoothelin-	Smoothelin-	Q8WWW1	28%	262	582
B3.			100%	201	1013
		-	%86	1107	1256
			27%	271	480
-			79%	532	996
 			44%	954	1052
astx (Q9P059) HSPC323		Q9P059	71%	332	562
(FRAGMENT)).		85%	148	462
WUblastx (Q8VD01) Hypothetical	pothetical	Q8VD01	46%	8	586

	609	757	444	903	352	421	244	274	1051	397
	31	298	145	46	170	107	62	2	212	332 130
	49%	83%	82.8	100%	20.3	%88	20.4	%16	%86	45%
	Q8VD01	09н3С0	PF00085	pir T12471 T12471	PF01569	б9Н929	PF01569	09 н929	Q9NR71	О9лнЕ3
61.8 kDa protein.	(Q8VD01) Hypothetical 61.8 kDa protein.	(Q9H3C0) PRO0898.	PFAM: Thioredoxin	hypothetical protein DKFZp564E1962.1 - human (fragment)	PFAM: PAP2 superfamily	(Q9H929) CDNA FLJ13055 FIS, CLONE NT2RP3001538, WEAKLY SIMILAR TO HYP	PFAM: PAP2 superfamily	(Q9H929) CDNA FLJ13055 FIS, CLONE NT2RP3001538, WEAKLY SIMILAR TO HYP	(Q9NR71) MITOCHONDRIAL CERAMIDASE.	(Q9JHE3) NERUTAL CERAMIDASE
.64	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64
	792	290	291		293		692		294	770
	880047	527402	610018		1172046		1035153		836041	600362
	HKMLP68	HKMND01	HL2AC08		HLCND09		HLCND09		HLDBE54	HLDBE54

				CERAMIDASE).				
HLDBE54	800678	771	HMMER 2.1.1	PFAM: Renal dipeptidase	PF01244	466.8	352	1410
			WUblastx .64	(Q9H4A9) PUTATIVE DIPEPTIDASE.	Q9H4A9	100%	133	1590
HLDBX13	815665	295	WUblastx .64	(Q9H387) PRO2550.	Q9Н387	%92 %92	1764 1815	1681
HLDNA86	1352197	296	WUblastx .64	(Q9BQB6) UNKNOWN (PROTEIN FOR MGC:11276) (PROTEIN FOR IMAGE:3455200).	Q9BQB6	100%	238	726
HLDNA86	535730	772	WUblastx 64	(Q9BQB6) UNKNOWN (PROTEIN FOR	ОЭВОВе	72%	326	424
				MGC:11276) (PROTEIN FOR IMAGE:3455200).		100%	45	218
HLDOW79	847396	298	WUblastx .64	(AAH24441) Hypothetical 37.8 kDa protein.	AAH24441	83%	10	669
HLDQC46	847397	299	WUblastx .64	(Q9BXJ8) TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR ALPHA	Q9BXJ8	100%	28	423
HLDQR62	753742	300	WUblastx .64	(Q9NQW2) PROGRESSIVE ANKYLOSIS-LIKE PROTEIN.	Q9NQW2	100%	41 376	382 1002
HLDQU79	740755	301	WUblastx .64	(O75477) KE04P.	075477	100%	105	1142
HLDRM43	846330	302	WUblastx	(Q96NZ9) Proline-rich	6ZN96O	100%	24	476

	919	278	571	335	636 616	559	406	572 701	704
	164	340 599	224	610	571	∞	296	54 675	9
	100%	38%	81%	100%	95%	999	%98	65% 100%	77%
	62N96D	О9Н743	Q9WVC2	pir JH0319 A31767	096N65	pir JC7367 JC7367	Q9NQZ1	AAH24408	Q8WU84
acidic protein.	(Q96NZ9) Proline-rich acidic protein.	(Q9H743) CDNA: FLJ21394 FIS, CLONE COL03536.	(Q9WVC2) LY- 6/NEUROTOXIN HOMOLOG (ADULT MALE HIPPOCAMPUS CDNA, RIKEN	macrophage inflammatory protein 1-beta precursor [validated] - human	(Q96N65) CDNA FLJ31349 fis, clone MESAN2000092, moderately similar to	second peroxisomal thioesterase - human	(Q9NQZI) HEPATOCELLULAR CARCINOMA ASSOCIATED PROTEIN TD26.	(AAH24408) Hypothetical 20.3 kDa protein (Fragment)	(Q8WU84) Hypothetical
.64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx
	773	303	304	776	307	309	310	777	311
	638939	647430	460467	894001	791828	520375	1307726	619979	853614
	HLDRM43	HLDRP33	HLHFP03	HLHFR58	нглсо90	HLQBE09	HLQDR48	HLQDR48	HLTAU74

				(Fragment).				
HLTEJ06	543017	314	WUblastx .64	(AAL78047) Envelope protein.	AAL78047	32%	173	490
HLTHG37	787530	316	WUblastx	(AAH01258) N-	AAH01258	100%	096	1070
		÷	.64	acetylglucosamine- phosphate mutase.		93%	7	955
HLTHG37	743169	778	WUblastx	(Q9NTT5) DJ202D23.2	Q9NTT5	100%	640	335
			.04	(FRAGMENT).				
HLWAA17	629552	317	WUblastx	(Q9NY26) IRT1	Q9NY26	94%	226	096
		<u></u>	.64	PROTEIN (SIMILAR TO		100%	82	123
				REGULATED				
		·	!	TRANSPORTER-LIK				
HLWAA88	588485	318	WUblastx	(Q9H8L6) CDNA	978H6D	%66	683	1768
			.64	FLJ13465 FIS, CLONE	•	%66	295	969
				PLACE1003493,		40%	781	855
				WEAKLY SIMILAR TO		42%	440	517
				END		92%	35	322
HLWAA88	769166	611	WUblastx	(Q9H8L6) CDNA	978Н6О	%56	1567	1629
			.64	FLJ13465 FIS, CLONE		93%	1487	1573
				PLACE1003493,		 %86	51	1493
		<u></u>		WEAKLY SIMILAR TO				-
	9	,		END				
HLWAD77	653513	319	WUblastx 64	(Q9GZP9) F-LAN-1 (HYPOTHETICAL	Q9GZP9	%66	29	745
				TRANSMEMBRANE		•		
! !				PROTEIN SBBI53).				
HLWAE11	783071	320	HMMER 2.1.1	PFAM: C1q domain	PF00386	44.4	403	682

861	1147	420	1263	40	495	969	664	408	829	503	1006	1326	1663	643	1594	1331	1475	722	1173		1127
28	449	139	1003	14	19	396	503	100	470	333	38	166	1448	563	1445	1260	1251	594	10		9
%66	%8 <i>L</i>	78%	%16	100%	83%	30%	41%	78%	79%	28%	%66	%62	100%	42%	23%	37%	%06	%69	84%		%9L
Q9BXI9	Q9NRG9										Q9BY87							Q96MM0	69CUS9		AAH06651
(Q9BXI9) COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-RELATED PROTEIN.	(Q9NRG9) GL003	(ADRACALIN) (AAAS	PROTEIN)	(UNKNOWN)	(PROTEIN FOR MGC:						(Q9BY87)	PROACROSIN	BINDING PROTEIN	SP32 PRECURSOR.				(Q96MM0) CDNA FLJ32172 fis, clone PLACE6000555.	(Q9CUS9) 4833416I09RIK	PROTEIN (FRAGMENT)	(AAH06651) Similar to hypothetical protein
WUblastx .64	WUblastx	.64									WUblastx	.64						WUblastx .64	WUblastx .64		WUblastx .64
	321										322							323	325		326
	587270										658702							1045194	765310		609161
	HLWA022										HLWAY54							HLWBH18	HLWBK05		HLWBY76

				FLJ23153				
HLYAN59	553507	781	WUblastx	(AAL 79706) Hypothetical	AAL79706	85%	624	719
			.64	9.4 kDa protein.		93%	639	728
				1		82%	617	721
HLYAZ61	1352163	332	WUblastx	(014626) PROBABLE G	H963_HUMAN	100%	1	855
			.64	PROTEIN-COUPLED RECEPTOR H963			***	
HLYAZ61	423998	782	HMMER	PFAM: 7 transmembrane	PF00001	71.8	280	-283
			2.1.1	receptor (rhodopsin family)				
			WUblastx	(O14626) PROBABLE G	H963 HUMAN	%86		846
			.64	PROTEIN-COUPLED	1			
				RECEPTOR H963.				
HLYES38	638042	334	WUblastx	(095662) POT. ORF VI	095662	81%	743	856
			.64	(FRAGMENT).		72%	281	313
						72%	306	524
						75%	466	735
						33%	145	243
HMADS41	596831	335	WUblastx	(AAH07725) Ceroid-	AAH07725	95%	186	449
			.64	lipofuscinosis, neuronal 8 (epile		100%	427	1041
HMADU73	1352177	336	WUblastx 64	(Q9EPE8) LOW-	Q9ЕРЕ8	87%	491	2626
			-	LIPOPROTEIN				
				RECEPTOR-RELATED PROTEIN 9.				
HMADU73	467053	783	WUblastx	(Q9EPE8) LOW-	О9ЕРЕ8	78%	115	294
			+	LIPOPROTEIN				
				RECEPTOR-RELATED				

1 1
WOULDSTAND (Q2 1 0.02) AINTIGEN .64 NY-CO-38.
HMMER PFAM: Mitochondrial 2.1.1
+-
.64 Mitochondrial uncoupling protein 5 long
WUblastx (Q9H728) CDNA:
blastx
.64 FLJ21463 FIS, CLONE COL04765.
WUblastx (Q9BGV8)
.64 HYPOTHETICAL 10.0 KDA PROTEIN.
WUblastx (Q9GZW0) DJ604K5.1
.64 (15 KDA SELENOPROTEIN)
WUblastx (095662) POT. ORF VI
.64 (FRAGMENT)
WUblastx (Q9H8K5) CDNA
PLACE1004815

1225	1346	2556	3024	879	2550	2622	834	2600		2555	3023	878	2549	2621	833	845			104	721	221	402	844	379	216	112
1341	1414	958	2488	376	2341	2494	712	2490		957	2487	375	2340	2493	711	69			09	107	183	229	338	500	109	62
%99	%09 %09	56%	36%	40%	35%	27%	40%	45.8		%95	36%	40%	35%	27%	40%	%68			73%	%66	100%	72%	100%	%86	94%	82%
Q9H743		09VZF8	,					PF00400		Q9VZF8						69ЕQН8			Q9BT67		Q9BT67	,	!	Q9BT67		
(Q9H743) CDNA:	FLJ21394 FIS, CLONE	(O9VZF8) CG1332	PROTEIN.					PFAM: WD domain, G-	beta repeat	(Q9VZF8) CG1332	PROTEIN.					(Q9EQH8) NEDD4 WW	DOMAIN-BINDING	FROIEIN 3 (FRAGMENT).	(Q9BT67) UNKNOWN	(PROTEIN FOR MGC·10924)	(09BT67) UNKNOWN	(PROTEIN FOR	MGC:10924).	(Q9BT67) UNKNOWN	(PROTEIN FOR	MGC:10924).
Jblastx	49:	WUblastx	.64					HMMER	2.1.1	WUblastx	.64					WUblastx	.64		WUblastx	.64	WUblastx	.64		WUblastx	.64	
357		358						787								359			788		789			790		
799540		1301451						994998								812208			723302		778820			674913		
HMSKC04		HMTBI36						HMTBI36								HMUAP70			HMUAP70		HMUAP70			HMUAP70		

60 104 107 583	60 104 106 720	61 207 187 300 333 449	647 549 473 345	42 1442	542 143842 596	 861 929 523 717 548 862 	319 453 428 769 651 839 903 1517	331 366 177 323 318 371	585 457	277
73% 1	86% 99%	100% 34% 1 97% 3	61% 6	%99	58% 5	78% 8 39% 5 44% 5	97% 3 66% 4 87% 6 99% 9	66% 3 54% 1 61% 3	65% 5	48%
Q9BT67	Q9BT67	Q96MX0	Q9P1C6	Q8VCP9	Q8VCP9	pir E41925 E41925	096914	Q26195	Q8WYX2	Q9H7Z0
(Q9BT67) UNKNOWN (PROTEIN FOR	(Q9BT67) UNKNOWN (PROTEIN FOR	MGC:10924). (Q96MX0) CDNA FLJ31762 fis, clone NT2RI2007754, weakly similar to INT	(Q9P1C6) PRO2738.	(Q8VCP9) RIKEN cDNA 1200003C23 gene.	(Q8VCP9) RIKEN cDNA 1200003C23 gene.	hypothetical protein 3 - human	(Q969J4) Lipocalin-1 interacting membrane receptor (Lipocalin-interac	(Q26195) PVA1 GENE.	(Q8WYX2) Hypothetical 14.1 kDa protein.	(Q9H7Z0) CDNA
WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx
791	792	361	793	363	794	365	366	367	368	369
646810	381964	638159	542061	1308287	794987	1036397	753337	460611	577013	410107
HMUAP70	HMUAP70	HMWEB02	HMWF002	HMWGY65	HMWGY65	HNEEB45	HNFFC43	HNFIU96	HNFJF07	HNFJH45

	206	706	617	557	695	2	487	861	116	715	610	725	561	945	734		857	663	701	10/		744	953		695		653	332
	12	12	492	492	486	190	537	965	1021	198	999	615	454	1028	919		973	098	001	1/0		577	714		522		7.0	334
	33%	31%	70%	34%	25%	36%	762	87%	53%	20%	73%	54%	%99	64%	62%		53%	71%	7017	0//0		38%	28%		%69		7007	16%
	Q96EF8							AAK55521		1	Q9N083			Q9HBS7			Q9H743		0000274	1200ch		096MM0	,		Q9NX85		000140	060448
HEMBB1000554.	(Q96EF8) Unknown	(protein for MGC:21495).						(AAK55521) PRO0764.		!	(Q9N083) UNNAMED	PORTEIN PRODUCT.		(Q9HBS7)	HYPOTHETICAL 14.2	KDA PROTEIN.	(Q9H743) CDNA:	FLJ21394 FIS, CLONE	COLUSSO.	(K)DOZH)	KDA PROTEIN.	(096MM0) CDNA	FLJ32172 fis, clone	PLACE6000555.	(Q9NX85) CDNA	FLJ20378 FIS, CLONE	NAIA030.	(O60448) NEURONAL
	Jblastx	.64						WUblastx	.64	!	WUblastx	.64	<u>.</u>	WUblastx	.64		WUblastx	.64	WI The Locator	_	<u>.</u>	├	.64	_	WUblastx	.64		WUblastx
	370							378			381			383			385		207	/00		388			399		100	402
	561488							499076			519120		:	561568			604891		02/1057	0.740.7		836064			463568		043400	843488
	HNGAK47							HNGEP09			HNGIJ31		!	HNGJE50			HNGJP69		UNICENIO	CONTRIBUTION		HNGOM56			HNHF029		TRITODAG	HNHOD46

921	713	894	498	625	917	792	915	791	595	552	462	839	1195					1037		1316		010	017			495	377		176
949	645	844	331	353	828	721	781	558	401	283	379	486	173		-	•		282		1111	<u> </u>	5	60			370	12		252
%95	999	52%	73%	26%	%05	30°C	48%	20%	35%	31%	20%	61%	100%	-		-		137.5		100%			7.67			%56	100%		57%
													095400					PF00001		Q9H1Y3		100001	PF00001			Q9H1Y3			AAH24118
THREAD PROTEIN	AD7C-NTP.												(095400) CD2	CYTOPLASMIC	DOMAIN BINDING	PROTEIN (CD2	ANTIGEN CYTOPLA	PFAM: 7 transmembrane	receptor (rhodopsin family)	(Q9H1Y3) DJ317G22.2	(ENCEPHALOPSIN)	(PANOPSIN).	PFAM: / transmembrane	receptor (rhodopsin	family)	(Q9H1Y3) DJ317G22.2	(ENCEPHALOPSIN)	(PANOPSIN).	(AAH24118) Similar to
.64					-								WUblastx	.64				HMMER	2.1.1	WUblastx	.64	411	HMMEK	2.1.1		WUblastx	.64		WUblastx
			_								11		405					406				000	807						407
					<u>.</u>								570877					1160395					855575						700627
													HNTBI57					HNTCE26					HNICE70						HNTNC20

	644	1236	969	803	931	969	863	662	922	1276	1356	1517	1157	1201	892	584	1198	551	537	329	389	329	581	1523	1076	201		295
	51	1204	54	99	824	42	99	48	416	635	1078	1482	1101	539	530	228	755	84	379	15	66	54	99	1485	1017	356	-	420
	%02	63%	37%	31%	29%	28%	30%	36%	30%	73%	762	41%	20%	78%	26%	36%	26%	73%	33%	32%	34%	30%	25%	42%	40%	61%		71%
	8ASX60	,																								Q9GMX5		Q9Н387
Unknown (protein for IMAGE:44	(09XSV8) SCO-	SPONDIN	(FRAGMENT)																							(Q9GMX5)	HYPOTHETICAL 12.9 KDA PROTEIN.	(Q9H387) PRO2550.
.64	WUblastx	.64																								WUblastx	.64	WUblastx
	409	<u> </u>															_									804		411
	1041383																						,,,			897950		520201
	HNTSV18	01101111																								HNTSY18		HOACB38

419	663	493	1021			1042		520			278			619		643			325	261	,	696		781	-		
589	743	099	1119			725	-	657			370	276		455		149			89	316		133		104			
77%	74%	%/9	100%			83%		%09	_		36%	54%		54.1		%06			%96	93%		31%		100%		,	
	Q9N083		Q9H1S5			Q8WZ36		Q9GMP5			pir S23650 S23650			PF00093		094769			094769			pir/118967/118967		Q9Y2Y6			
	(Q9N083) UNNAMED	PORTEIN PRODUCT.	(Q9H1S5) BA110H4.2 (SIMILAR TO	MEMBRANE	PROTEIN).	(Q8WZ36) Hypothetical	11.9 kDa protein.	(Q9GMP5)	HYPOTHETICAL 6.6	KDA PROTEIN.	retrovirus-related	hypothetical protein II -	human 1	PFAM: von Willebrand	factor type C domain	(094769)	EXTRACELLULAR	MATRIX PROTEIN.	(094769)	EXTRACELLULAR	MAIRIX PROTEIN.	hypothetical protein	elegans	(Q9Y2Y6) TADA1	PROTEIN	(DKFZP564K1964	FROIEIN).
.64	WUblastx	.64	WUblastx .64			WUblastx	.64	WUblastx	.64		WUblastx	.64		HMMER	2.1.1	WUblastx	.64		WUblastx	.64	1	W Ublastx 64	5	WUblastx	.64		
	414		415			416		417			420	_		421					807			422		423			
	520348	`	422913			790333		579256			834907			768325					509951			//1878		634994			
	HODDN65		HODDN92			НОББО08		HODDW40			HODGE68			HOEBK34					HOEBK34	,		HOEBZ89		HOEDB32			

1535	1449	216	1507	1969	1300	555	1460	434	2001	489	629	505	383	546	704	1500	815		1499	737		857		877
933	7	142	695	1496	1163	10	1419	303	1945	127	555	206	54	109	549	43	288		42	318		72		1584
%66	39%	22	%16	94%	36%	100%	21%	78%	100%	44%	34%	30%	78%	30%	%96	85%	189.8		85%	162.2		81%		81%
Q8WY86	800960	PF00560	00006d													MTN3_HUMAN	PF00092		MTN3_HUMAN	PF00092		MTN3_HUMAN		MTN3_HUMAN
WUblastx (Q8WY86) PP3686.	(Q960D8) SD05564p.	PFAM: Leucine Rich Repeat	(Q9C000) NAC-BETA	SPLICE VARIANT.												(O15232) MATRILIN-3 PRECURSOR.	PFAM: von Willebrand	ractor type A domain	(015232) MATRILIN-3 PRECURSOR.	PFAM: von Willebrand	factor type A domain	(015232) MATRILIN-3	PRECURSOR.	(015232) MATRILIN-3
WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx	.64		_										WUblastx .64	HMMER	2.1.1	WUblastx .64	HMMER	2.1.1	WUblastx	.64	WUblastx
424	425	426														427	608			810				811
1036480	748236	833079														1184465	919896			906694		!		902639
HOEDE28	НОЕДН84	HOEFV61														НОҒМQ33	НОҒМQ33			HOFMQ33				НОҒМQ33

			.64	PRECURSOR.				
НОҒМQ33 70	702186	812	WUblastx	(Q8WUF2) Hypothetical	Q8WUF2	%88	937	911
			.64	23.7 kDa protein.		%66	914	327
HOFMT75 91	911180	428	HMMER	PFAM: Eukaryotic	PF00026	619	290	1303
			2.1.1	aspartyl protease				
			WUblastx	cathepsin D (EC 3.4.23.5)	pir A25771 KHHUD	%18	83	1312
			.64	precursor [validated] -				-
				human				
HOFMT75 90	905365	813	WUblastx	cathepsin D (EC 3.4.23.5)	pir A25771 KHHUD	%59	83	361
			.64	precursor [validated] -				-
				human				
HOFMT75 89	892308	814	WUblastx	cathepsin D (EC 3.4.23.5)	pir A25771 KHHUD	%88	1494	757
			.64	precursor [validated] -			<u> </u>	
				human				
HOFMT75 89	892291	815	HMMER	PFAM: Eukaryotic	PF00026	496.2	336	1232
			2.1.1	aspartyl protease				
 			WUblastx	cathepsin D (EC 3.4.23.5)	pir A25771 KHHUD	%66	129	1232
			.64	precursor [validated] -				
				human				
HOFND85 84	847424	430	HMMER	PFAM: Cadherin domain	PF00028	256	905	1180
-			WUblastx	(AAK51617)	AAK51617	83%	167	2047
			49.	Protocadherin-beta7.		30%	425	1858
HOFOC33 11	1186156	432	WUblastx	clusterin precursor - dog	pir A40018 A40018	%69	1022	1414
			.64			81%	115	1086
НОГОСЗЗ 96	967554	817	HMMER	PFAM: Clusterin	PF01093	236.4	81	395
-			2.1.1	1	. 14 4001914 40019	440/	27.2	157
			WUblastx	clusterin precursor - dog	pir A40018 A40018	44%	3/3	453
1			.04			91%	10	393
HOFOC33 87	878690	818	HMMER	PFAM: Clusterin	PF01093	236.6	81	395

	453	432	1415	432	1087	257	36	-733	55	812		311		918	341	414	920	819		130		
	373	92	1023	9/	440	583	839	-422	5	42		192		316	18	64	411	2291		35		
	91%	301.2	77%	%56	%98	84%	77%	74.6	52%	87%		22.3		87%	\ \%0 <i>L</i>	%9L	84%	100%		100%		
	pir A40018 A40018	PF01093	pir A40018 A40018			pir A40018 A40018	pir A40018 A40018	PF00428	pir/A27125/R5HUP0			PF00112		BAB22302		CAC09370		BAB55004		Q8WUD4		
	clusterin precursor - dog	PFAM: Clusterin	clusterin precursor - dog			clusterin precursor - dog	clusterin precursor - dog	PFAM: 60s Acidic ribosomal protein	acidic ribosomal protein	P0, cytosolic [validated] -	human		cysteine protease	(BAB22302) Adult male	kidney cDNA, RIKEN full-lengt	(CAC09370) DJ543J19.3	(cathepsin Z).	(BAB55004) CDNA	FLJ14357 fis, clone HEMBA1000005, h	(Q8WUD4) Similar to	RIKEN cDNA	2700094L05 gene.
2.1.1	WUblastx .64	HMMER 2.1.1	WUblastx	.64		WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx	.64		HMMER	2.1.1	WUblastx	.64	WUblastx	.64	WUblastx	.64	WUblastx	.64	
		618				820	821	822	 			433				823		825		434		
		905734				902326	885140	806819				931871				907073		878863		579891		
		НОГОСЗЗ				НОГОСЗЗ	НОГОС33	НОГОСЗЗ				HOFOC73				HOFOC73		HOFOC73		HOGAW62		

1622	389	1616	382	125	81	1534	1264	1214	1161	872	477	1383	1388	952	719	2356	2493	707	1/85	721	1702	
378	57	1533	89	51	52	371	1214	1161	514	813	22	31	36	1017	931	2294	2374	348	9/9	170	221	
%66	%16	%76	%16	44%	20%	%66	%9 <i>L</i>	%88	100%	%001	 %96	%66	%66	%65	74%	%12	%09	94%	9//6	100%	%001	
Q969N2		Q969N2					Q9Y386			Q96BI3		Q9NY68	69NY68	Q9H728		Q9UIS0		Q8WUJ3		060565	095965	
(Q969N2) Phosphatidyl	inositol glycan class T precursor (Hypothetical	(Q969N2) Phosphatidyl	inositol glycan class T	precursor (Hypothetical			(Q9Y386) CGI-78	PROTEIN.		(Q96BI3) Hypothetical	29.0 kDa protein (CGI-78 protein).	(Q9NY68) CTL2 PROTEIN.	(Q9NY68) CTL2 PROTEIN.	(Q9H728) CDNA:	FLJ21463 FIS, CLONE COL04765.	(Q9UI50) PRO0657	(FRAGMENT).	(Q8WUJ3) Hypothetical	110.4 kDa protein.	(060565) GREMLIN (DRM).	(095965) TEN	INTEGRIN EGF-LIKE REPEAT DOMAINS
WUblastx	.64	WUblastx	.64				WUblastx	.64		WUblastx	.64	WUblastx .64	WUblastx .64	WUblastx	.64	WUblastx	.64	WUblastx	.64	WUblastx .64	WUblastx	.64
435		826					436			827		437	828	829		438		439		441	443	
745445		664499					895880			902295		919898	907118	867965	·····	833080		896809		873264	827481	
HOGCK20		HOGCK20					HOGCK63			HOGCK63		HOGCS52	HOGCS52	HOGCS52		HOHBB49		НОНВС68		HOHBY44	НОНСН55	

	1712	1576	1621	1426	292		-			539	···		176					593	544		82	537			-1633		1927	
	1623	416	230	326	136					288			144					468	143		2	46			-647		99	
	100%	31%	%66	40%	100%					95.1			%86					85%	%98		21%	100%			697.3		100%	
	095965				Q9NWM8					PF00254			69NWM8					6Y8Q6Q			Q9NUTS				PF01747		pir JW0087 JW0087	
PROTEIN PRECURSOR.	(095965) TEN	INTEGRIN EGF-LIKE	REPEAT DOMAINS	PROTEIN PRECURSOR.	(Q9NWM8) CDNA	FLJ20731 FIS, CLONE	HEP10272	(HYPOTHETICAL 24.2	KDA PRO	PFAM: FKBP-type	peptidyl-prolyl cis-trans	Isomerases	(Q9NWM8) CDNA	FLJ20731 FIS, CLONE	HEP10272	(HYPOTHETICAL 24.2	KDA PRO	(Q9D8Y9)	1810018L05RIK	PROTEIN.	(Q9NUT5) CDNA	FLJ11152 FIS, CLONE	PLACE1006901	(FRAGMENT).	PFAM: ATP-sulfurylase		3'-phosphoadenosine-5'-	phosphosulfate synthetase
	WUblastx	.64			WUblastx	.64				HMMER	2.1.1		WUblastx	.64				WUblastx	.64		WUblastx	.64			HMMER	2.1.1	WUblastx	.64
	832				444					833								445			446				447			
	815682				1299928					457167								854234			545809				614040			
	нонсн55				HONAH29					HONAH29								HOSDJ25			HOSEG51				HOSFD58			

383513 835	astx		pir JW0087 JW0087	100%	99	1927
.64	phosphosulfate synthetase - human	ite synthetase				
HMM 2.1.1	IER PFAM: Reprolysin family propeptide	olysin family	PF01562	76.2	216	-20
WUbla	lastx (P97857) ADAM-TS	AM-TS 1	ATS1_MOUSE	81%	208	3408
<u>+</u>	3.4.24) (A	N(E)				
WUblas	lastx (09NUX1) CDNA	DNA	O9NUX1	87%	4	585
.64		S, CLONE	,			
WUblastx	1	FERUS-	035360	73%	-	1818
.64	OVARY SPECIFIC	SCIFIC			-	
	PUTATIVE					
	TRANSMEMBRANE PROTEIN.	ABRANE				
HMMER 2.1.1	PFAM: CUB domain	domain	PF00431	146.9	452	778
WUblastx	x (035360) UTERUS-	TERUS-	035360	67%	8	928
.64	OVARY SPECIFIC	SCIFIC		75%	918	1814
	PUTATIVE					
	TRANSMEMBRANE PROTEIN.	MBRANE				
WUblastx 64	 	IMILAR TO	Q9BWJ9	%96	99	154
· }	(NERVE TISSUE)	SSUE)				
WUblastx	 	Adrenal	AAH07349	%26	57	257
40.	I wand protelli	A 7-(3/4				

HPFDG48	542227	458	WUblastx	WUblastx (Q9Y6E5) HSPC024-ISO. Q9Y6E5	09Y6E5	%06	564	623
			.64		•	88%	313	387
HPIAQ68	833082	459	WUblastx .64	(Q95LL4) Hypothetical 13.9 kDa protein.	Q95LL4	46%	902	1174
HPIBO15	1310868	460		(Q9CQS3) 1110018M03RIK PROTEIN.	Q9CQS3	93%	128	757
HPIBO15	590741	840	WUblastx .64	(Q9CQS3) 1110018M03RIK PROTEIN.	Q9CQS3	88% 95% 97%	127 507 401	402 722 508
HPICB53	1042309	461	WUblastx .64	(Q9NX17) CDNA FLJ20489 FIS, CLONE KAT08285.	09NX17	74%	1138	848
HPJCL22	1146674	463	WUblastx .64	(Q9GKV3) HYPOTHETICAL 41.8 KDA PROTEIN.	Q9GKV3	97% 27% 75%	1420 210 2701	2508 338 2823
HPJCL22	1034817	845	WUblastx .64	(Q9VWN8) CG7307 PROTEIN.	8NMA6O	69%	64 468	348
HPJCL22	1046434	846	WUblastx .64	(Q9H8F3) CDNA FLJ13680 FIS, CLONE PLACE2000007, HIGHLY SIMILAR TO HOM	Q9H8F3	94% 81%	346	582
HPJCW04	696685	464	WUblastx .64	(Q9P195) PRO1722.	Q9P195	39%	1278	1093 1263
HPMAI22	635491	466	WUblastx .64	(Q9CX19) 9430073N08RIK PROTEIN.	Q9CX19	54%	147	572
НРОАС69	396804	469	WUblastx .64	(075592) PROTEIN ASSOCIATED WITH	075592	100%	202 76	297

PF00481 336.4 Q9HAY8 99% Q9HAY8 98% Q9H8I7 99% Q9H8I7 96% Q9H728 64% Q9H756 55% AAH25678 100% Q9HA75 63% Q9HA75 63%					MYC.		100%	3	200
2.1.1 phosphatase 2C	HPRBC80	829136	470	HMMER	PFAM: Protein	PF00481	336.4	157	957
WUblastx (Q9HAY8) SER/THR				2.1.1	phosphatase 2C				
Coloparation Colo			·	WUblastx	(Q9HAY8) SER/THR	Q9НАУ8	%66	94	1254
PHOSPHATASE TYPE 2C BETA 2 ISOFORM PROTEIN PLASE TYPE PLASE TYPE TYPE TYPE TYPE PLASE TYPE TYPE TYPE TYPE TYPE TYPE TYPE TYP				.64	PROTEIN				
CAROTEIN PROTEIN PROTEIN PROTEIN					PHOSPHATASE TYPE				
CHRUTEIN CPHATS SERTTHR COHAYS S8%					2C BETA 2 ISOFORM				
720095 851 WUblastx (Q9HAY8) SEK/IHK Q9HAY8 98% PHOSPHATASE TYPE 2 C BETA 2 ISOFORM (PROTEIN PHOSPHATASE TYPE 2 C BETA 2 ISOFORM (PROTEIN PLACE1009493. PLAC				,	(PKUI EIN			,	
Cartest	HPRBC80	720095	851	WUblastx	(Q9HAY8) SER/THR	Q9HAY8	%86	m	284
PHOSPHATASE TYPE 2C BETA 2 ISOFORM PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PLACE1009493. 644 PLACE1009493. PLACE1009493. 644 PLACE1009493. PLACE1009493. 644 PLACE1009493. PLACE1009493. 644 PLACE1009493. PLACE1009493. 644 Protein (Fragment). PLACE1009493. 644 PLACE1009493. PLACE1009493. PLACE1009493. 644 PLACE1009493. PLACE1009493. PLACE1009493. PAB84985 PLACE1009493.				.	PROTEIN				
CC BETA 2 ISOFORM PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PLACE1009493. PLACE1049493. PLACE104949493. PLACE1049494949494949494949499494993. PLACE1049494949494949494949494949494949494949					PHOSPHATASE TYPE			-	
753282 471 WUblastx (Q9H817) CDNA Q9H817 99% 64 FLJ13593 FIS, CLONE PLACE1009493. 99% 634353 473 WUblastx (BAB84985) FLJ00232 BAB84985 96% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx (Q9H728) Similar to AAH25678 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 64 FLJ1212 FIS, CLONE 64 FLJ1212 FIS, CLONE 69HA75 48%					2C BETA 2 ISOFORM			<u>, , , , , , , , , , , , , , , , , , , </u>	
753282 471 WUblastx (Q9H8I7) CDNA Q9H8I7 99% 634353 473 WUblastx (BAB84985) FLJ00232 BAB84985 96% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 658717 478 WUblastx (AAH25678) Similar to G84 AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 64%					(PROTEIN				
634353 FLJ13593 FIS, CLONE PLACE1009493. 634353 473 WUblastx (BAB84985) FLJ00232 BAB84985 96% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H763 FIS, CLONE) COL04765. 34% 658717 478 WUblastx (AAH25678) Similar to 64 AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS, CLONE 48% 63%	HPRBF19	753282	471	WUblastx	(Q9H8I7) CDNA	718H6D	%66	15	632
634353 473 WUblastx (BAB84985) FLJ00232 BAB84985 96% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx hypothetical protein 3 - pir[E41925 E41925 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 48%				49.	FLJ13593 FIS, CLONE				
634353 473 WUblastx (BAB84985) FLJ00232 BAB84985 96% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx hypothetical protein 3 - pirlE41925 E41925 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 658717 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 48%					PLACE1009493.				
722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx hypothetical protein 3 - pir[E41925]E41925 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS. CLONE R8% 48%	HPTVX32	634353	473	WUblastx	(BAB84985) FLJ00232	BAB84985	%96	103	543
722246 476 WUblastx (Q9H728) CDNA: Q9H728 64% 64 FLJ21463 FIS, CLONE Q9H728 64% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx hypothetical protein 3 - pir/E41925/E41925 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 654 putative. 64 FLJ12122 FIS, CLONE 69HA75 69HA75				.64	protein (Fragment).				
709662 854 FLJ21463 FIS, CLONE 67% 709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 585702 477 WUblastx hypothetical protein 3 - pir[E41925 E41925 34% 658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS, CLONE 48%	HPWDJ42	722246	476	WUblastx	(Q9H728) CDNA:	Q9H728	64%	1100	1026
709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% 64 FLJ21463 FIS, CLONE 67% 67% 585702 477 WUblastx hypothetical protein 3 - pir[E41925 E41925 34% 658717 478 WUblastx (AAH25678) Similar to an analysis AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS, CLONE 48%				.64	FLJ21463 FIS, CLONE		%29	1332	1102
709662 854 WUblastx (Q9H728) CDNA: Q9H728 64% .64 FLJ21463 FIS, CLONE 67% 67% 585702 477 WUblastx hypothetical protein 3 - pir E41925 E41925 34% 658717 478 WUblastx (AAH25678) Similar to putative. AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS, CLONE 48%					COL04765.				
585702 477 WUblastx hypothetical protein 3 - pir E41925 E41925 34% 658717 478 WUblastx (Q9HA75) CDNA AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS. CLONE 48%	HPWDJ42	709662	854	WUblastx	(Q9H728) CDNA:	Q9H728	64%	1100	1026
585702 477 WUblastx hypothetical protein 3 - pir/E41925/E41925 34% 658717 478 WUblastx (AAH25678) Similar to putative. AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS. CLONE 48%				.64	FLJ21463 FIS, CLONE		%19	1332	1102
585702 477 WUblastx hypothetical protein 3 - pir/E41925/E41925 34% 658717 478 WUblastx (AAH25678) Similar to an interventative. AAH25678 100% 882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 64 FLJ12122 FIS. CLONE 48%					COL04765.				
658717 478 WUblastx (AAH25678) Similar to AAH25678 100% 64 ELJ12122 FIS. CLONE 55% 658 human 55% 658 human 65% 658	HPZAB47	585702	477	WUblastx	hypothetical protein 3 -	pir E41925 E41925	34%	1132	884
658717 478 WUblastx (AAH25678) Similar to AAH25678 100% .64 putative. Q9HA75 Q9HA75 63% 882176 479 WUblastx (Q9HA75) CDNA 63% .64 FLJ12122 FIS. CLONE 48%				.64	human		55%	1296	1183
882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% 63% 64 FLJ12122 FIS. CLONE	HRAAB15	658717	478	WUblastx	(AAH25678) Similar to	AAH25678	100%	111	511
882176 479 WUblastx (Q9HA75) CDNA Q9HA75 63% FLJ12122 FIS. CLONE 48%			!	.64	putative.				
FLJ12122 FIS. CLONE	HRABA80	882176	479	WUblastx	(Q9HA75) CDNA	Q9HA75	63%	647	629
				.64	FLJ12122 FIS, CLONE		48%	144	371

				MAMMA1000129.		93%	247	507
HRABA80	588460	856	WUblastx	(Q9HA75) CDNA	Q9HA75	63%	633	999
			.64	FLJ12122 FIS, CLONE	,	48%	130	357
				MAMMA1000129.		92%	233	493
HRACD15	871221	480	WUblastx	(AAH08084)	AAH08084	%86	1452	253
			.64	Hypothetical 50.4 kDa protein.				
HRACD15	706332	857	WUblastx	(AAH08084)	AAH08084	82%	1649	1581
			.64	Hypothetical 50.4 kDa protein.		%86	1596	253
HRACD80	1309774	481	WUblastx	(CAC37630) Fibulin-6	CAC37630	44%	200	1866
			.64	(Fragment).		36%	37	1446
						45%	1282	1920
-						42%	1291	1584
_						47%	1291	1530
HRACD80	882163	858	HMMER 2.1.1	PFAM: EGF-like domain	PF00008	64.3	1337	1441
			WUblastx	(CAC37630) Fibulin-6	CAC37630	44%	\$69	1861
			.64	(Fragment).		37%	32	1441
						45%	1277	1915
						42%	1286	1579
						47%	1286	1525
HRDDV47	637650	482	WUblastx .64	(Q9VXD6) CG9723 PROTEIN.	90XX6Q	27%	224	964
HRDFD27	567004	483	WUblastx	(Q9N032) UNNAMED	Q9N032	47%	629	476
			.64	PROTEIN PRODUCT.				
HROAJ03	567005	484	WUblastx	(Q96A82) CDNA	Q96A82	%88	7	186
			-64	FLJ30106 fis, clone				
				BNGH41000190, weakly				
				similar to Kat				

678 707 605 682	546 701	23 403	1055 933 1218 1030	967 674	1386 1102	92 313	1662 1573 1580 1338	362 793	299 796 791 1084	60 1256	225 470
%08 76%	63%	95%	70%	67%	81%	100%	%09 20%	163.5	%86 %66	100%	18.7
85IN6Ò	Q9BE22	Q9CZR4	Q9H728	Q9NX85	О9Н387	Q9NRX6	Q9N083	PF00194	CAHE_HUMAN	Q9Y279	PF00047
(Q9UIS8) PRO0483 PROTEIN.	(Q9BE22) HYPOTHETICAL 13.4 KDA PROTEIN.	(Q9CZR4) 2700018N07RIK PROTEIN.	(Q9H728) CDNA: FLJ21463 FIS, CLONE COL04765.	(Q9NX85) CDNA FLJ20378 FIS, CLONE KAIA0536.	(Q9H387) PRO2550.	(Q9NRX6) PROTEIN X 013.	(Q9N083) UNNAMED PORTEIN PRODUCT.	PFAM: Eukaryotic-type carbonic anhydrase	(Q9ULX7) CARBONIC ANHYDRASE XIV PRECURSOR (EC 4.2.1.1) (CAR	(Q9Y279) Z39IG PROTEIN PRECURSOR.	PFAM: Immunoglobulin domain
astx	WUblastx 64	WUblastx .64	WUblastx .64	WUblastx .64	astx	WUblastx .64	 		WUblastx .64	ļ	HMMER 2.1.1
486	488	489	490	491	492	493	494	496		497	862
531973	490879	545459	561435	460527	580872	545051	604143	692358		1352253	625998
HSATR82	HSAUL82	HSAVH65	HSAVK10	HSAWD74	HSAWZ41	HSAXA83	HSAYB43	HSDAJ46		HSDEK49	HSDEK49

1040	542	336	335	1352	702	590	539	590	702	209
444	126	4	6	1645	4	57	9	57	10	6
%88	%66	%86	%68	77%	%66	65%	65%	64%	100%	100%
Q9Y279		pir[T17101 T17101	pir T17101 T17101	Q9NX85	Q9BZW5	Q9BVS2	Q9BVS2	Q9BVS2	060245	O9NX00
(Q9Y279) Z39IG	PROTEIN PRECURSOR.	probable voltage-activated cation channel - rat	probable voltage-activated cation channel - rat	(Q9NX85) CDNA FLJ20378 FIS, CLONE KAIA0536.	(Q9BZW5) TRANSMEMBRANE 6 SUPERFAMILY MEMBER 1.	(Q9BVS2) UNKNOWN (PROTEIN FOR IMAGE:3451448) (FRAGMENT).	(Q9BVS2) UNKNOWN (PROTEIN FOR IMAGE:3451448) (FRAGMENT).	(Q9BVS2) UNKNOWN (PROTEIN FOR IMAGE:3451448) (FRAGMENT).	(O60245) PCDH7 (BH-PCDH)A.	(Q9NX00) CDNA FLJ20512 FIS, CLONE KAT09739.
WUblastx	.64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64
		499	863	200	501	503	864	865	909	507
		1352287	704101	589974	795252	1036471	904821	905623	545057	651375
		HSDEZ20	HSDEZ20	HSDFW45	HSDJA15	HSDJL42	HSDJL42	HSDJL42	HSDSE75	HSDZR57

598	1201	362	884	916	966	1764 1526	1760	286	734	1037
S	431	108 350	153	251	1289	1829	1825 1782	38	699	54
%66	%001	100%	100%	100%	74%	%59 %65	%59 %65	%96	23.4	%66
Q9NV22	О9Н6Н4	О9Н6Н4	881960	096.188	Ф9Н728	AAK55521	AAK55521	Q96D15	PF00036	Q96D15
(Q9NV22) CDNA FLJ10983 FIS, CLONE PLACE1001781, WEAKLY SIMILAR TO PRO	(Q9H6H4) CDNA: FLJ22277 FIS, CLONE HRC03740.	(Q9H6H4) CDNA: FLJ22277 FIS, CLONE HRC03740.	(Q96J88) Putative breast epithelial stromal interaction protein.	(Q96J88) Putative breast epithelial stromal interaction protein.	t .	(AAK55521) PRO0764.	(AAK55521) PRO0764.	(Q96D15) Hypothetical 37.5 kDa protein.		(Q96D15) Hypothetical 37.5 kDa protein.
WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64
208	509	298	510	898	511	512	698	513	870	
612823	1352191	514183	1352248	612877	589447	1033671	902162	1304677	661698	
HSHAX21	HSIAS17	HSIAS17	HSICV24	HSICV24	HSIDJ81	HSIDX71	HSIDX71	HSJBQ79	HSJBQ79	

586	906	243	3635	1789	1792	1791	1790	1670	1671	1136	102	740	-326		744	241	740	
32	49	49 234	982	1601	1718	127	1716	6	1597	1071	28	75	-30		6L	98	216	
97%	%66	%86 %96	83%	%09	52%	73%	32%	%69	32%	36%	%96	100%	92		100%	75%	%98	
Q96D15	Q9H5G5	Q9H5G5	BAB85613	BAB85613				BAB85613		pir T02229 T02229		Q96DA4	PF00254		Q96DA4	054998		
(Q96D15) Hypothetical 37.5 kDa protein.	(Q9H5G5) CDNA: FLJ23462 FIS, CLONE HSI08475.	(Q9H5G5) CDNA: FLJ23462 FIS, CLONE HSI08475.	(BAB85613) URB.	(BAB85613) URB.				(BAB85613) URB.	,	protein BYJ15 - common	tobacco (fragment)	(Q96DA4) FK506- binding protein.	PFAM: FKBP-type	peptidyl-prolyl cis-trans isomerases	(Q96DA4) FK506- binding protein.	(054998) FK506-	BINDING PROTEIN 7	PRECURSOR (EC 5.2.1.8) (FKRP-23) (PE
	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx 64				WUblastx	.64	WUblastx	.64	WUblastx .64	HMMER	2.1.1	WUblastx .64	WUblastx	.64	
871	514	872	515	873				874		628		522	088			881		
371784	702021	413210	1352409	1074734				872570		906498		1306702	602258			401251		
HSJBQ79	HSKCP69	HSKCP69	HSKDA27	HSKDA27				HSKDA27		HSODE04		HSQE084	HSQEO84			HSOE084	,	

368 399 69 266 251 257 1105	2161	2155	946	939	949	633	171	901
15 301 10 174 78 99 99	344	338	62	55	161	589	356	101
83% 40% 72% 41% 32% 87%	100%	100%	81%	100%	76%	73%	85%	93%
080N60	Q96F18	Q96FI8	О9Н400	О9Н400	О9Н400	095LL0	pir T42734 T42734	Q9H7F4
(Q9NQ80) ASPIC PRECURSOR.	(Q96FI8) Unknown (protein for MGC:9160).	(Q96FI8) Unknown (protein for MGC:9160).	(Q9H400) DJ583P15.4.1 (NOVEL PROTEIN (TRANSLATION OF CDNA FLJ20406 (E	(Q9H400) DJ583P15.4.1 (NOVEL PROTEIN (TRANSLATION OF CDNA FLJ20406 (E	(Q9H400) DJ583P15.4.1 (NOVEL PROTEIN (TRANSLATION OF CDNA FLJ20406 (E	(Q95LL0) Hypothetical 11.3 kDa protein.	cytoplasmic linker protein CLIP-115 - rat	(Q9H7F4) CDNA: FLJ20979 FIS, CLONE ADSU01938.
WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64
524	526	882	528	883	884	530	533	534
566879	1352343	845666	1306937	745409	716424	413246	898965	944388
HSSDX51	HSSGD52	HSSGD52	HSSJC35	HSSJC35	HSSJC35	HSUBW09	HSVBU91	HSXCG83

726	860	454	2170	2064	838	1713 544 544 2514 750 3090 654 670 1458 2119 2052	871
4	585 762	383	371	1945	50	889 272 2101 478 3007 289 608 1015 2005 2573	458
%86	56% 55%	6.7.9	%96	70%	100%	98% 55% 100% 92% 42% 33% 56%	%69
Q9H7F4	О9Н728	PF00560	Q96CX1	Q96NR6	Q9NVZ3	FHOS_HUMAN	FHOS HUMAN
(Q9H7F4) CDNA: FLJ20979 FIS, CLONE ADSU01938.	(Q9H728) CDNA: FLJ21463 FIS, CLONE COL04765.	PFAM: Leucine Rich Repeat	(Q96CX1) Similar to RIKEN cDNA 2610528G05 gene (Fragment).	(Q96NR6) CDNA FLJ30278 fis, clone BRACE2002755.	(Q9NVZ3) CDNA FLJ10420 FIS, CLONE NT2RP1000170.	(Q9Y613) FH1/FH2 DOMAINS- CONTAINING PROTEIN (FORMIN HOMOLOG	(Q9Y613) FH1/FH2
WUblastx .64	WUblastx .64		WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx
885	536	537		688	068	540	891
830673	886200	847358		902235	882732	1177537	862063
HSXCG83	HSXGI47	HSYAV50		HSYAZ50	HSYAZ50	HSYAZ63	HSYAZ63

			.64	DOMAINS-		95%	1364	1447
				CONTAINING		73%	930	1298
				PROTEIN (FORMIN		52%	362	418
				HOMOLOG		33%	387	476
					:	100%	14	70
HSYBG37	1056317	541	WUblastx .64	hypothetical protein c316G12.3 [imported] -	pir T45062 T45062	100%	47	961
HSYBG37	581098	892	WUblastx	hypothetical protein	pir T45062 T45062	100%	48	962
			40.	c310012.3 [imported] - human				
HSZAF47	1352172	542	WUblastx	(Q9BXJ2)	Q9BXJ2	100%	106	972
			.64	COMPLEMENT-CIQ				
				FACTOR-RELATED				, ,
				PROTEIN.				
HSZAF47	456551	893	HMMER	PFAM: Collagen triple	PF01391	54.4	299	478
			2.1.1	helix repeat (20 copies)				
			WUblastx	(Q9BXJ2)	Q9BXJ2	%76	107	926
			.64	COMPLEMENT-C1Q				
				TUMOR NECROSIS				-
				FACTOR-RELATED				
HT3SF53	884170	543	WUblastx	(Q9H5B4) DJ470L14.2.1	Q9H5B4	100%	312	533
			.64	(STAUFÉN (RNA	,			
				BINDING PROTEIN)				
				ISOFORM 1).				
HT5GJ57	1299921	544	WUblastx	(Q9GZY6) CDNA	9XZD6Ò	%68	105	833
			.64	FLJ11237 FIS, CLONE				- '
				r LACE 1000331		7	7	

	856	5 1117	2 412 8 959	0 585 8 952 4 488		2 617	2 768	7 298	9 257	3 231	3 327
	122	155	92 408	490 548 84	319	372	142	17		43	253
	84%	%98	100%	%46 %46	78%	78%	%92	%86	100%	46%	100%
	09GZY6	Q8WV10	Q96A28	Q96A28	Q9D412	Q9D4I2	Q9D412	Q9BX79	AAH25354	Q95L10	Q9NP89
(WBSCR5) (WBSCR15 PROT	(Q9GZY6) CDNA FLJ11237 FIS, CLONE PLACE1008531 (WBSCR5) (WBSCR15 PROT	(Q8WV10) Hypothetical 38.4 kDa protein.	(Q96A28) CD84-H1 (CD2 FAMILY 10).	(Q96A28) CD84-H1 (CD2 FAMILY 10).	(Q9D412) 4932408F18RIK PROTEIN.	(Q9D412) 4932408F18RIK PROTEIN.	(Q9D412) 4932408F18RIK PROTEIN.	(Q9BX79) STRA6 ISOFORM 1.	(AAH25354) Similar to putative.	(Q95LI0) Epididymis- specific protein ESP13.6.	(Q9NP89)
	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx
	894	545	546	895	547	968	897	548	549	550	551
	740767	844835	753289	457172	1018291	882919	864120	396835	866485	462221	587326
	HT5GJ57	HTADW91	HTADX17	HTADX17	HTAEE28	HTAEE28	HTAEE28	HTDAF28	HTEAF65	HTEBI28	HTEDF80

			.64	HYPOTHETICAL 42.7		91%	353	451
				KDA PROTEIN		100%	852	1073
				(FRAGMENT).		75%	112	210
						%86	869	856
						%99	450	863
HTEDY42	1352193	552	WUblastx	(Q96L06) Similar to	90Т96Ò	100%	19	717
			.64	RIKEN cDNA				
HTEDY42	519372	868	HMMER	PFAM: SCP-like	PF00188	20	86-	-193
			2.1.1	extracellular protein				
			WUblastx	(Q96L06) Similar to	907960	100%	19	231
			.64	RIKEN cDNA		33%	576	719
			•	1700011E04 gene.		94%	224	700
HTEGI42	908143	555	WUblastx	(Q8WW43) Hypothetical	Q8WW43	%66	26	961
			.64	28.5 kDa protein.				
HTEGI42	904624	668	WUblastx	(Q8WW43) Hypothetical	Q8WW43	%66	145	915
			.64	28.5 kDa protein.				
HTEGI42	850770	006	WUblastx	(AAL93028) Hypothetical	AAL93028	%9L	154	26
			.64	26.9 kDa protein.		462	154	38
						%6L	154	38
						19%	154	38
						19%	154	38
	·				·	72%	153	25
						81%	155	45
						83%	156	46
	··					%96	155	72
						85%	154	62
						79%	154	38
HTEGI42	847564	901	WUblastx	(Q14288)	Q14288	95%	503	429
			.64	HYPOTHETICAL		%19	444	

				PROTEIN				
				(FRAGMENT).				
HTEHR24	835894	929	WUblastx	(Q9HBV2) SPERM	Q9HBV2	%92	84	656
			.64	MEMBRANE ANTIGEN SMARC32.				
HTEHR24	513039	903	WUblastx	(Q9HBV2) SPERM	Q9HBV2	%91	41	529
			.64	MEMBRANE ANTIGEN	,	100%	692	922
				SMARC32.		%96	514	693
HTEHU93	722254	557	WUblastx	(O60676) CYSTATIN-	CRES_HUMAN	100%	188	613
			.64	RELATED			-	
				EPIDIDYMAL				
				SPERMATOGENIC				
:				PROTEIN			-	
нтени93	423009	904	HMMER 2.1.1	PFAM: Cystatin domain	PF00031	31.7	35	-105
			WUblastx	(060676) CYSTATIN-	CRES HUMAN	100%	504	614
			.64		l	78%	187	552
				SPERMATOGENIC				
				PROTEIN				
HTEJN13	1352272	999	WUblastx	(Q9BWY1) BA552M11.5	Q9BWY1	100%	158	193
			.64	(NOVEL PROTEIN)		100%	351	622
7. 4. 1.			3	(FKAGMENI).				
HIEJNI3	658744	506	WUblastx	(Q9DAR9)	Q9DAR9	- - - - - - - - - - - - - - - - - - -	525	743
			.64	1700001D09RIK PROTEIN.		77%	163	516
HTEJN13	381941	906	WUblastx	(Q9HBK8) AD026.	Q9HBK8	92%	161	229
			.64	1		94%	214	633
HTEPG70	834931	562	WUblastx	(075295) R27328_2.	075295	93%	23	268
			.64					

672 661	566	517	968	941	911	691	455 1069	2495	423 1016 2503	482
502 149	258	846	552	99	1045	533	3 449	30	40 423 911	360
55%	44%	52%	160.3	%68	%99	62.1	98% 100%	100%	95% 98% 94%	100%
O9NZX5	Q9DAL9	Q9NX17	PF00175	бэлнбэ	Q9P1H3	PF00909	Q9UBD6	901X6	09UJX6	Q9NV11
WUblastx (Q9NZX5) HSPC062.	(Q9DAL9) 1700007K09RIK PROTEIN.	(Q9NX17) CDNA FLJ20489 FIS, CLONE KAT08285.	PFAM: Oxidoreductase FAD/NAD-binding domain	(Q9UHQ9) NADH- CYTOCHROME B5 REDUCTASE ISOFORM.	(Q9P1H3) PRO1438.	PFAM: Ammonium Transporter Family	(Q9UBD6) RH TYPE C GLYCOPROTEIN (TUMOR-RELATED PROTEIN DRC2).	(Q9UJX6) ANAPHASE- PROMOTING COMPLEX SUBUNIT 2.	(Q9UJX6) ANAPHASE- PROMOTING COMPLEX SUBUNIT 2.	(Q9NV11) CDNA
WUblastx .64	WUblastx .64	WUblastx .64	HMMER 2.1.1	WUblastx .64		HMMER 2.1.1	WUblastx .64	WUblastx .64	WUblastx .64	WUblastx
563	564	292	567		268	569		570	606	571
597467	410582	919911	693652		772559	706618		1040047	873355	519329
HTGAU75	HTGEP89	HTHBG43	HTHDJ94		HTHDS25	HTJMA95		HTJML75	HTJML75	HTLAA40

217			1177		86				499	534	346			289			869			619			149		434	773	932	1007
14	176	840	1112		961				543	908	17			1			12			2			3		36	528	312	330
100%	%86	93%	81%		%76				%99	68%	%66			%88			%06			%06			81%		%66	100%	32%	%86
	Q96M29				Q96M29				Q8WTZ3		01SN6O			Q9D2V1			997/269			997/260			Q9NY64		Q96L02		Q96QH1	,
FLJ11004 FIS, CLONE PLACE1002941.	(Q96M29) CDNA	FLJ32871 fis, clone	TESTI2003914, weakly	similar to Tek	(Q96M29) CDNA	FLJ32871 fis, clone	TESTI2003914, weakly	similar to Tek	(Q8WTZ3) Hypothetical	27.2 kDa protein.	(Q9NSI0) PRED58	PROTEIN	(FRAGMENT).	(Q9D2V1)	2310009N05RIK	PROTEIN.	(060766)	2310009N05RIK	PROTEIN.	(907060)	2310009N05RIK	PROTEIN.	(Q9NY64) GLUCOSE	TRANSPORTER.	(Q96L02) Hypothetical	24.5 kDa protein.	(Q96QH1) NB1	Glandratein pregureor
.64	WUblastx	.64			WUblastx	.64			WUblastx	.64	WUblastx	.64		WUblastx	.64		WUblastx	.64		WUblastx	.64		WUblastx	.64	WUblastx	.64	WUblastx	77
	572				910				573		574			575			911			912			576		577		578	
	902187				885431				634852	,	460583			1352310			791409			608317			1035130		838460		833906	
	HTLBE23				HTLBE23				HTLEP53		HTLFE42			HTLFE57			HTLFE57			HTLFE57			HTLGE31		HTLHY14		HTLIT32	-

HTLIV19	1046341	579	WUblastx	(096LS9) CDNA	6ST960	20%	119	172
			.64	FLJ25101 fis, clone	,	%69	178	315
				CBR01328.				
HTODK73	526021	582	WUblastx	(Q9H8P2) CDNA	248H6Q	93%	404	448
			.64	FLJ13348 FIS, CLONE		100%	292	707
				OVARC1002127,		71%	433	474
				WEAKLY SIMILAR TO		43%	4	189
				SOD		61%	418	519
						%08	21	401
HTOHM15	1028538	585	WUblastx	(Q9NVL9) CDNA	67AN6Ò	%96	1641	1718
			.64	FLJ10649 FIS, CLONE		100%	1507	1650
				NT2RP2005835,				
				WEAKLY SIMILAR TO				
				SHP				
HTOHM15	848200	915	HMMER 2.1.1	PFAM: UBX domain	PF00789	9.76	794	1033
			WUblastx	(Q9H102) DJ776F14.1	Q9H102	100%	37	129
			.64	(ORTHOLOG OF		%16	95	1036
				MOUSE P47).				
HTOHM15	848196	916	WUblastx	(Q9NVL9) CDNA	67AN6O	%96	1307	1384
			.64	FLJ10649 FIS, CLONE		100%	1173	1316
				NT2RP2005835,				
				WEAKLY SIMILAR TO SHP				
HTOIZ02	847904	917	WUblastx	ataxin 7 - human	pir T09193 T09193	%66	714	1196
			.64			31%	437	619
						47%	303	359
						28%	224	718
						%26	2	736
HTOJA73	797108	685	WUblastx	(Q9H387) PRO2550.	Q9Н387	63%	1044	955

1046	644	757	1263	1387	1269	1243	543	762	1072	2180	-1276	1592		875	510	498	238	525	889	280	192	77	273
1246	745	870	178	302	1198	92	106	727	1007	1644	926-	1488		792	370	7	179	379	542	179	4	12	76
74%	73%	78%	100%	%66	62%	%66	%02	83%	29%	100%	6:59	82%		100%	92%	27%	35%	37%	79%	%02	9692	45%	57%
	Q9HA67		096893	096893	Q9BWS9		Q9Y2C7				PF00622	095014		Q9BTF2								Q9D7W4	
	(Q9HA67) CDNA	FLJ12155 FIS, CLONE MAMMA1000472.	(Q96S93) Hypothetical 41.7 kDa protein.	(Q96S93) Hypothetical 41.7 kDa protein.	(Q9BWS9) UNKNOWN	(PROTEIN FOR MGC:3234).	(Q9Y2C7)	BUTYROPHILIN LIKE	RECEPTOR.		PFAM: SPRY domain	(095014) WUGSC:H DJ0855D21.2	PROTEIN.	(Q9BTF2) REC8P, A	MEIOTIC	RECOMBINATION	AND SISTER	CHROMATID	COHESION			(Q9D7W4)	2210021G21RIK
.64	WUblastx	.64	WUblastx .64	WUblastx .64	WUblastx	.64	WUblastx	.64			HMMER 2.1.1	WUblastx .64		WUblastx	.64							WUblastx	.64
	590		591	918	616		593				920	594		595								969	
	545067		1317835	581435	396459		812763				909573	429618		714344								1310814	
	HTOJK60		HTPBW79.	HTPBW79	HTPBW79		HTTDB46				HTTDB46	HTWCT03	! ! !	HTWDF76								HTXAJ12	

				PROTEIN.				
HTXAJ12	567434	921	WUblastx	(AAH24685) Similar to	AAH24685	100%	6	95
			.64	transmembrane 4		%86	62	267
				supertamily m				
HTXDW56	695765	869	WUblastx	(Q96A54) Similar to CGI-	Q96A54	%66	7	819
			.64	45 protein (Hypothetical				
				42.6 kDa protein).				
HTXFL30	620001	599	WUblastx	(Q96KR5)	Q96KR5	%86	305	1990
			.64	Leishmanolysin-like		100%	30	89
				peptidase, variant 2 (EC		100%	213	299
				3.4.24.36).		100%	89	94
HTXKF95	891275	009	WUblastx	(AAH08360) Similar to	AAH08360	84%	324	644
			.64	hypothetical protein		95%	81	203
				FLJ22376				
HTXKF95	834438	923	WUblastx	(AAH08360) Similar to	AAH08360	%001	2	553
			.64	hypothetical protein			-	
				FLJ22376				
HTXKP61	824083	601	WUblastx	(Q9H0S8)	8S0H6D	83%	3	1064
			.64	HYPOTHETICAL 53.0				
				KDA PROTEIN.				
HUDBZ89	1352211	602	WUblastx	(Q9VH80) CG16908	09VН80	23%	271	1530
			.64	PROTEIN.				
HUDBZ89	562791	924	WUblastx	(Q9VH80) CG16908	09VH80	22%	7	327
			.64	PROTEIN.		33%	330	641
HUFEF62	645101	604	WUblastx	hypothetical L1 protein	pir JU0033 JU0033	81%	355	308
			.64	(third intron of gene TS) -		84%	314	12
				human				
HUFEF62	260089	976	WUblastx	hypothetical L1 protein	pir JU0033 JU0033	81%	347	300
			.64	(third intron of gene TS) -		84%	306	4
				human				

738	269	479	462	1300	597	571	370	1338	710	316	216			1845		1069	1622	1666	459	219	700	748	620	673	581	453
286	144	462	55	131	520	200	152	1039	597	134	6			280		281	1566	1067	1	43	317	623	87	695	72	346
100%	94%	100%	93%	82%	30%	33%	73%	100%	34%	28%	%001			100%		%66	42%	100%	77%	79%	100%	38%	24%	40%	25%	62.8
62N960	6ZN96Ò	6ZN96Ò	,	Q96AA2							VDP_HUMAN			FBX7_HUMAN		AAH08361			AAH08361			Q9V6L4	,	Q9V6L4		PF01699
(Q96NZ9) Proline-rich acidic protein.	(Q96NZ9) Proline-rich acidic protein.	(Q96NZ9) Proline-rich	acidic protein.	(Q96AA2) Obscurin.				_			(O60763) GENERAL	VESICULAR TPANSPOPT FACTOR	PI15 (TRANSCYTO	(Q9Y3II) F-BOX ONLY	PROTEIN 7.	(AAH08361) F-box only	protein 7.	•	(AAH08361) F-box only	protein 7.		(Q9V6L4) CG12251	PROTEIN.	(Q9V6L4) CG12251	PROTEIN.	PFAM: Sodium/calcium
	WUblastx .64	WUblastx	.64	WUblastx	.64						WUblastx			WUblastx	.64	WUblastx	.64		WUblastx	.64		WUblastx	.64	WUblastx	.64	HMMER
605	927	928		909							209			809		929			930			609		931		610
1352424	1300737	603538		694590							566762			1352367		883176			655372			1194812		1044491		838626
HUKAH51	HUKAH51	HUKAH51		HUKBT29							HUSIG64			HUSXS50		HUSXS50			HUSXS50			HVARW53		HVARW53		HWAAD63

			2.1.1	exchanger protein				
			WUblastx	(09НС58)	09НС58	%59	229	813
			.64	SODIUM/CALCIUM				
				EXCHANGER NCKX3.				
HWAAD63	833089	932	HMMER	PFAM: Sodium/calcium	PF01699	37.8	346	453
			2.1.1	exchanger protein				
			WUblastx	(Q9HC58)	Q9HC58	%8 <i>L</i>	229	453
			.64	SODIUM/CALCIUM		55%	429	969
				EXCHANGER NCKX3.		72%	533	814
HWAAD63	793875	933	HMMER	PFAM: Sodium/calcium	PF01699	113.7	336	773
	!		2.1.1	exchanger protein				
			WUblastx	(Q9HC58)	Q9HC58	%9L	219	908
			.64	SODIUM/CALCIUM				
				EXCHANGER NCKX3.				
HWABY10	768334	612	WUblastx	(Q96AW1) Hypothetical	Q96AW1	100%	165	999
			.64	19.2 kDa protein.				
HWBA062	838164	614	HMMER	PFAM: Immunoglobulin	PF00047	27.9	202	405
			2.1.1	domain				
			WUblastx	(Q14288)	Q14288	45%	1331	1618
			.64	HYPOTHETICAL		%99	1158	1334
				PROTEIN		%59	1847	1894
				(FRAGMENT).		55%	1594	1839
HWBAO62	625914	934	WUblastx	(Q14288)	Q14288	43%	1358	1645
			.64	HYPOTHETICAL		62%	1874	1921
	١			PROTEIN		%99	1185	1361
				(FRAGMENT).		25%	1621	1866
HWBAR88	836469	615	WUblastx	(Q9Y2C2)	Q9Y2C2	%96	215	786
			.64	DERMATAN/CHONDR		100%	107	241
				OITIN SULFATE 2-		83%	856	1050
				SULFOTRANSFERASE.				

597		433		066			143	78		133	89	1070			1048			196		5133							3038
37		104	36	32			340	158		330	148	707	100		206			2784	952	5801	4499	4550	528	3727	5062	4123	1774
100%		170.2	1000/	100%			27%	85%		27%	85%	2000	9370		93%		1	%66	20%	%16	75%	47%	75%	29%	75%	37%	7000
BAB55294		PF00255	D 4 D 5 5 3 0 4	BAB33294			0MM96Q			096MM0		0011700	(%0U%)		Q9NR73	,		096858	,							-	
(BAB55294) CDNA	FLJ14777 fis, clone NT2RP4000259, w	PFAM: Glutathione peroxidases	O A DESCOUN CONTA	(BABSS294) CDNA	FLJ14777 fis, clone	NT2RP4000259, w	(Q96MM0) CDNA	FLJ32172 fis, clone	PLACE6000555.	(Q96MM0) CDNA	FLJ32172 fis, clone pr ACF6000555	COULOS CONTA	(Q9H087) CDINA:	FLJ22494 FIS, CLOINE HRC11131.	(Q9NR73)	MACROPHAGE ABC	TRANSPORTER.	(Q96S58) ABCA-SSN.									
WUblastx	.64	HMMER 2.1.1	11/1 11-10-24-1	w U blastx	.64		WUblastx	.64		WUblastx	.64	11.11.1.	W U DIASIX	,	WUblastx	.64		WUblastx	.64								
616		935					617			936		017	010		619			938									
1093347		886210					846382			646977		1250075	1332203		907063			290206									
HWBCB89		HWBCB89					HWBCP79			HWBCP79		ocarativity (HWBDF28		HWBFE57			HWBFE57									

						37%	1293	532
						36%	2152	2003
						52%	5014	4964
						31%	254	123
						29%	5233	5132
						70%	4881	4561
						94%	4462	2783
						%16	5169	4423
			,			20%	2049	1708
HWBFE57	876136	939	WUblastx	(Q14287)	Q14287	28%	252	13
			.04	HYPOTHETICAL PROTEIN				
				(FRAGMENT).				
HWDAH38	1028519	621	WUblastx	(Q9NX85) CDNA	Q9NX85	71%	943	1119
			.64	FLJ20378 FIS, CLONE		%69	1113	1250
				KAIA0536.		48%	1600	1340
HWDAH38	889281	941	WUblastx	(Q64150) NUCLEAR	064150	%09	795	673
			.64	LOCALIZATION				
				SIGNAL BINDING				
				PROTEIN.				
HWHGP71	995431	622	HMMER	PFAM: 7 transmembrane	PF00001	31.2	389	992
			2.1.1	receptor (rhodopsin family)				. .
			WUblastx	leukotriene B4 receptor 2,	pir JC7356 JC7356	%95	992	1020
			.64	BLTR2 - human		47%	434	484
						74%	101	992
HWHGP71	839250	942	blastx.2	(AJ278605) leukotriene	emb CAB96134.1	77%	106	465
				B4 receptor 2 [Homo		100%	555	770
				sapiens		28%	922	1036
HWHGQ49	1352257	623	WUblastx	(AAH25278) Androgen	AAH25278	100%	26	902

			.64	induced protein.				
HWHGQ49	636080	943	WUblastx	(AAH25278) Androgen	AAH25278	93%	42	725
			.64	induced protein.				
HWHGU54	569569	624	HMMER	PFAM: Serpins (serine	PF00079	501.1	277	1377
			2.1.1	protease inhibitors)				
			WUblastx	(AAL99574) OL-64	AAL99574	62%	145	1377
			.64	protein.				
HWHGZ51	886212	625	WUblastx	(Q9UJ74)	Q9UJ74	100%	33	1070
			.64	HYPOTHETICAL 36.0				
				KDA PROTEIN (C4.4A			-	
				PROTEIN).				
HWHHL34	805642	979	WUblastx	(075915) JWA PROTEIN	075915	100%	131	694
			.64	(HSPC127) (VITAMIN A				
				RESPONSIVE,				
				CYTOSKELETON RE				
HWHHL34	801943	944	WUblastx	(075915) JWA PROTEIN	075915	95%	53	613
			.64	(HSPC127) (VITAMIN A				
				RESPONSIVE,				
				CYTOSKELETON RE				
HWHHL34	341560	945	WUblastx	(075915) JWA PROTEIN	075915	100%	101	664
			.64	(HSPC127) (VITAMIN A				
				RESPONSIVE,				, .
				CYTOSKELETON RE				
HWLEV32	1032602	627	WUblastx	(O00378) PUTATIVE	000378	44%	684	535
			.64	P150.		38%	556	17
HWLEV32	873296	946	WUblastx	retrovirus-related reverse	pir/A25313 GNHUL1	%05	614	525
			.64	transcriptase pseudogene -		40%	510	7
				human				
HWLEV32	881710	947	WUblastx	(BAB85074) CDNA	BAB85074	%26	61	396
			.64	FLJ23835 fis, clone		-		

				KAIA2214.				
HWLEV32	846351	948	WUblastx	(BAB85074) CDNA	BAB85074	%66	2	409
			.64	FLJ23835 fis, clone		, · · ·		
				KAIA2214.				
HWLIH65	793713	628	HMMER	PFAM: Integral	PF01940	49.3	147	455
	- -		2.1.1	membrane protein				
			WUblastx	(AAH08596) Unknown	AAH08596	%86	81	623
1			2	(protein for MGC:16985).				
HYAAJ71	826754	630	WUblastx	(Q9NX17) CDNA	Q9NX17	62%	1147	1464
			.64	FLJ20489 FIS, CLONE				
				KAT08285.				
HUSBA88	895435	631	HMMER	PFAM: Glycosyl	PF01532	694	783	2102
			2.1.1	hydrolase family 47				
			WUblastx	(Q9UKM7) ALPHA 1,2-	Q9UKM7	94%	18	2114
			.64	MANNOSIDASE.				

RACE Protocol For Recovery of Full-Length Genes

Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation, therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or Sall, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dAtailing reaction which results in a polyT stretch that is difficult to sequence past.

An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (e.g., as described in columns 2 and 3 of Table 1A, and/or as set forth in Table 1B, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 1A and Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A and/or Table 1B (ATCC Deposit No:Z). A clone which is isolatable

from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A and/or Table 1B or Table 2, by procedures hereinafter further described, and others apparent to those skilled in the art.

Also provided in Table 1A and Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res. 16:*7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res. 17:*9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies 5:*58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus* 15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (ATCC Deposit No:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants,

splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in ATCC Deposit No:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, prosequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in ATCC Deposit No:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1C. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1C are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the

complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in ATCC Deposit No:Z.

Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1C column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1C column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1C, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1C, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1C, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1C, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1C, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). In additional embodiments, the above-described

polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1C which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1C, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1C which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1C, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1C, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1C, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1C, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). In additional embodiments, the abovedescribed polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1C which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1C, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1C, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1C column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary

strand(s) of the sequences delineated in the same row of Table 1C column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1C column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1C, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1C, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1C, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1C, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1C, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1C, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1C which correspond to the same Clone ID (see Table 1C, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A, Table 1B, or Table 1C) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1C, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A, Table 1B, or Table 1C) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of

SEQ ID NO:X correspond to the same row of column 6 of Table 1C. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1C are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1C are directly contiguous. Nucleic acids which

hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID (see Table 1C, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one—sequence in column 6 corresponding to the same contig sequence identifer SEQ ID NO:X (see Table 1C, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1C, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

Table 3

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the fifth column of Table 1A and/or the fourth column of Table 1B, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety

Table 3					
	SEQ				
cDNA	ÖN	Contig	EST D	sclaimer	
Clone ID	×	Ë	Range of a	Range of b	Accession Numbers
H2CBG48	=	745365	1	15 - 2797	AL536879, AL536880, AW974652, BF978951, AI761251, AI655763, AA307225, AA628063,
					AWU45561, AW576500, AI693821, BEU47125, AI129381, AI701013, AA651750, AW172561, AW530506 AW1085016 AA457150 AA65061 AI580600 AV680672 BE20614 AI500104
					. A.W.353500, A.W.083710, A.A.57130, A.G.05251, A.J.05262, A.V.000772, D. 052514, A.J.370174, A.W.085909, A.M.0716242, A.M.000008, A.M.05270, N.52070, A.M.293021, A.M.371342, B.F.891108, A.M.058439,
					BF946218, BF891008, AV689991, AV690900, A1458885, A1962506, H40784, A1364207, AA464514,
					AW994164, BF946219, AV656660, BF891112, AA336322, AA337109, AI824603, AA336509,
					AA336407, BF036975, AA337222, N46906, AA464515, AA319240, AA765507, AW361203,
					AA053434, AI928199, AW299270, AV713792, N50282, AA056762, BE708029, AW361192, W07762,
					AL513817, BE965014, Al866082, AL513723, Al689470, Al684244, Al866624, BF970652, AW024594,
					AL514691, BF525392, AL047100, AL513687, AI963763, AI925404, AL514473, BE966388, AI634249,
					A1241901, AA580663, AL513553, A1584130, AV727963, BF868489, A1973288, A1499570, A1638644,
					AI745684, AI765323, AI583065, AI909697, BG058398, BE964967, AL514085, BE966547, AI889818,
					A1890223, A1473536, AL036187, AI521799, BE892325, AL514145, AL046466, AI636811, AI540179,
					AW262983, AL513779, Al345415, BG110192, AV761267, AL514493, BG030785, BE879336,
					AI590043, AV696866, AI417790, AI698391, AW088628, AL514359, AI916419, AI433647, AI690536,
					AI690748, AW081383, AL514497, AL513755, BE965732, AL514455, AW129264, AI382670,
					AI689557, AI357940, AI277008, AA761608, AW079334, AI884318, ALS14047, AI493576, AI421903,
					BE967005, AI590227, AW105460, AI719817, AL037582, AL037602, AV682533, BF766531,
					AW161202, A1469505, A1491775, AW020397, A1744243, BE540578, A1953765, AW834282,
					BE966577, AL514867, AI635851, AW075382, BE962903, AL514871, AL514469, AL515195,
					BF309444, AV747571, A1873638, A1524724, A1440239, AL514899, BE967070, A1679550, A1345612,
					AL514457, BF039003, AA743354, BF792961, AL513911, AA631120, AW083374, AI284060,
					A1623179, BF791791, AL036705, AW827289, A1363741, BE966927, A1288305, BF895218,
					AL514155, BE966579, AW088899, Al345416, Al267185, BE964999, Al359787, AW189415,
					AI538850, AI301710, AW008226, AI341690, AI611743, AW198090, AI620302, AI683606, AL513951,
					AW078712, AL046618, BE964726, BG164558, AI540674, AI884469, AI539771, BF724420,
					BF970436, AI567846, AI862024, AI627866, AI696570, AW073677, AI362522, AI679891, AI678446,
					AL513781, BF981785, AL079799, BF727091, AI567625, BE888257, BG104845, AL515235,
					AI627893, AI559619, BG036506, AW500379, AI089970, AI270039, BG031894, AI932739, AI539042,
					AW007309, AI367210, AI933783, AI434731, AL445590.4, BC006159.1, AL050155.1, AL390154.1,
					BC001655.1, AK025435.1, BC000077.1, AB060876.1, AF218000.1, X82434.1, AK026885.1,
	_				AF232009.1, AL389935.1, AL137476.1, BC000632.1, AB048964.1, AL080154.1, AK026762.1,

AL137648.1, AK027102.1, AL137533.1, AL117587.1, AL117460.1, AR023530.1, AL157482.1, AL157488.1, AL156747.1, AF155827.1, AL137488.1, AL136747.1, AF155827.1, AL137288.1, AL136062.1, AL354776.15, AL157488.1, AL156747.1, AF155827.1, AL15768.1, AL0801491, BC0006414, AZ150015.1, BC0002473.1, BC0002473.1, BC0002473.1, BC0002473.1, BC0002671, AC004382.1, AF159615.1, AB056372.1, BC0002473.1, BC0002671, AC004382.1, AF159615.1, AB056372.1, BC0002473.1, BC0002671, AC004382.1, AC004382.1, AF159615.1, AB056372.1, BC0002473.1, BC00052671, AC004383.1, AL136850.1, AC0035991, AC025991, AL122100.1, AC004383.1, AL136850.1, AC003591.1, AC0035991.1, AC025991.1, AL122100.1, AC004382.1, AC004382.1, AC003998.1, ST771.1, AL137550.1, AL133619.1, AL1358983.1, AC024588.1, AC024388.1, AC024388.1, AC024382.1, AC024382.1, AC024382.1, AC024382.1, AL122104.1, BC000379.1, AC024932.1, AL13482.1, AC024932.1, AC024933.1, AC02493.1, AC024933.1, AC02493.1, AC02493.1, AC02493.1, AC02493.1, AC	BC002365.1, BC000253.1, BC006195.1, AL353594.13, BC006458.1, AR027164.1, AL136780.1, BC005890.1, AL136864.1, AL359618.1, BC007021.1, AK024570. 1.	1 - 445 15 - 459
		544957
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		H2MAC30

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H6EAB28	13	135222	1 - 1925	15 - 1939	AL537848, BE796835, BE793657, BE793638, BF968748, BE727036, BF316464, BE728420, BF314482, BE868759, BE793653, BF9968748, BE727036, BF316464, BE728420, BF314482, BE868759, BE407252, BE409490, BE276749, BE384252, BG235902, BE261749, BF125396, A1961321, A1001128, A1343334, AW135558, BE729783, AA777237, AA478021, A1623324, A1825954, BE220322, AL537847, AA232184, AA478177, BE220321, BE965762, BE276538, AA182540, A1085995, AA242851, BE621538, A1864561, AA308520, BG056114, A1872887, AA252149, D81546, H44644, R02178, BF093043, AA626640, BG149380, H43602, AA852699, AA449104, BE386947, BE727929, AA776508, AA583629, AA252298, BG111945, BF448098, BE314222, AC004840.3, AF239822.1, BC002918.1, A1289131.
H6EDF66	14	520498	1 - 526	15 - 540	
HABAG37	15	637942	1 - 640	15 - 654	AW245081, AI143992, AA495832, AI361951, AI090193, AI598190, AI380542, AI990174, AI859137, AA994262, AI350501, AI394639, AI086091, AI990481, AA293019, AW003834, AA976745, AI351614, AI202144, AA115762, AA253139, BE727402, R88936, N72164, AW237082, AW025153, R90773, AI766469, AI672360, BF718243, AA745682, AW134904, AA495776, AL119175, F23330, AA417706, AW274357, AW268196, R36266, AI913519, W00431, AA496881, BE252368, AA610858, AA417706, AW274357, AW268196, R36266, AI913519, W00431, AA496881, BE252368, AA610858, AA417588, AA133537, AI693690, BF339469, BG166654, BG164558, AW078929, AI473536, AL119399, AI345688, AL042544, AI539469, BG166654, BG164558, AW078929, AI473536, AI345688, AL042544, AI539771, AI288050, BF812961, AI472566, AA326898, AI866469, AI633125, AI698391, AI538564, AI915291, AW152182, AA248795, BF811804, AI88772, AW087934, AI570966, AI884318, AI933992, AW151714, AW051088, AW877289, AI61743, A1933903, AI8660608, BF812248, AI873633, AI801766, AI537677, AI492528, AI249962, BF871314, AI8660608, BF82127, AI24027, AI628254, AW168503, AW191844, W74529, AI610115, AW63834, BE965169, AI249877, A1963763, AI811344, AI870073, AI916419, AW5083832, AI537024, AI951950, BE843339, AW169790, AI610115, AW983382, AI640729, AI610729, AI811344, AI520785, BF814357, AI67349, AI67073, AI67074, AI67346, AR67248, AI67074, AI762073, AI67074, AI7673901, AI578484, BF86862, AW026882, AA502794, AI917963, AI54484, BF868927, AI54484, BF868927, AI67074, AI

BF222472, AI249946, AI590021, AI679891, AL046618, BF680133, AW188434, AI828574, AI625384, T69241, AW149311, AI690585, AI590227, AI630931, AI884469, AI281757, AI476478, AA835801, AI573032, AI500061, AI680162, AI567846, AI366900, AW081322, AI951868, AI583065, AI345745, AI536638, AI815232, AI434242, AW162214, AI659795, AI702406, AL038605, AW168795, AW080090, AI472536, AI659334, AW946864, AL043355, AV745810, AI866040, AI580190, AI583533, AI561231, BF812936, AW080590, AI472536, AI659334, AW946864, AL043355, AV745810, AI860640, AI580190, AI583533, AI561231, BF812936, BE543089, AI654750, AI923370, BF812938, AC005786.1, AF218008.1, AC005787.1, AL389935.1, AK025092.1, AL354776.15, AL035067.2, AK025435.1, BC004264.1, AK026462.1, BC004349.1, AL136850.1, AL080159.1, AL050149.1, AR026462.1, BC004349.1, AL136850.1, AL080159.1, AL137547.1, BC004356.1, AL080148.1, AL080159.1, AL050155.1, AL162083.1, AB0476371.1, AL137256.1, AL050155.1, AL162083.1, AB060912.1, AL049339.1, AK000418.1, AL080154.1, Z82022.1, BC007551.1, AL13688.1, BC009341.1, D83032.1, AL133645.1, BC002342.1, AL26056.1, AL26056.1, AL26056.1, AL26056.1, AL26056.1, AL26056.1, AL26056.1, AL080154.1, AL353956.1, AL137488.1, AL136622.1, U77594.1, AL110196. 1.	AI123694, AA203656, AV707802, BF575227, N77966, AW956121, N71852, BF732312, AI338999, AA704675, AI742966, AA176725, AV744696, AI039168, AA329423, AA680411, F10345, T85994, AV682639, AA731436, AV733262, AV733694, AA505796, AW959998, BF793146, H79631, R00088, BF978632, BG034327, AV716953, AW955313, BG032189, AV717860, AV716893, BF244606, AV733654, BG030662, AI802907, AA528524, AA973692, AA658895, AV714250, AV718258, AV716004, BF029739, F26324, AW772717, BE909294, AA370595, AI322630, AV718258, AV716004, BF029739, F26324, AW772717, BE909294, AA370595, AI322630, AV718258, AV716004, BF029799, AI126322, AA977864, R38777, AI093884, AW264528, AI351443, AA916014, AA359165, AA594324, AI682171, AA404535, BG033031, T90966, BF109665, BE551387, AI833308, AI814033, BF78181, BF035996, BF06505, F33601, BF216659, F33502, BE467615, AV738506, BE503802, AV763934, BG110890, AV742881, AV710956, BF965198, BG033031, T90966, R02459, F32392, BF248289, N64163, BF576733, AW872492, BE218579, BE539011, BE042987, BF978393, BF091038, AW009337, AA886535, BF738709, AI253328, AW268515, BF977850, H79632, AV764341, BF214426, BE184678, BE171856, BF382191, F77724, BF564110, F21702, BF24100, F26311, F27624, F31646, F24066, F30253, F21422, BF031636, AA340809, BF246303, F224016, N58379, AA706899, BE73786, AA340808, BF246303, F22361, BF212059, D19917, BF210763, A122059, BF0008551, AF0449571, AC0088594, 6
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					AL109855.16, AL139421.11, AC009131.6, AC004913.2, AC010422.7, AC009506.5, AC022415.5, AC002470.17, AL121869.19, AC006330.5, AL133215.16, AL031431.8, AC010513.6, AL353588.25,
			, -		U91326.1, AC073542.4, AC007220.4, AC007132.3, AP001726.1, AL133286.9, AL357558.6, AC022078.12, AP000047.1, AC011247.10, AC018751.30, AL034549.19, AP001724.1, AC008687.4,
					AP001415.1, AL163201.2, AC072061.8, AC008040.7, AC006515.7, X55931.1, AC005971.5,
					AL031904.1, AP001680.1, AP000017.2, AC004067.1, AC007845.12, AP001631.1, AC005006.2,
			_		AL137791.19, AC004166.12, AC004004.1, AL021453.1, AP001666.1, AF015720.2, AC011510.7, AC011479.6, AC007057.3, AC018828.3, AC040160.4, AF020803.2, AC035147.3, AL030997.1,
					AL161799.19, AC006947.2, AC000159.6, AL449106.15, AC021752.5, AC004965.2, AC012492.9, AB004907.1, AF312032.1, AF131215. 1.
HAGAI85	19	381942	1 - 1738	15 - 1752	AL526844, AL534504, AL532583, AL526885, AL534503, AL532762, BF791804, BF979873,
					AU139874, AV706645, AW952336, BF979324, AU139805, BE615117, AW189934, AU129651,
					AW3/2808, AU138184, AI613227, AW969233, AA834118, AI03/333, AW023337, AI610008, AV728299, AI460229, AU151734, AI676226, AA450163, BF217638, AI242616, R76281, AI004063,
					AA450100, AI095551, H46944, W05356, AI075684, W31703, T86800, AI339293, R85337, AA468695,
					H94753, H46945, AA323897, R77461, R77559, R26135, H43527, R80736, AA772424, H60113,
					R63353, H12406, H12407, R85338, R76558, R26349, R63354, A1609126, R68089, R68131, R80737,
					AW103602, AA745911, H59459, AI122795, Z41708, AI248729, AI800670, AW798408, BF931590,
				- 1	BF896996, BF733086, BE929484, BF903415, AV724914, U83461. 1.
HAGAM64		626997	1 - 2307	15 - 2321	BF925125, BF925123, BF925124, BF925118, BF925117, BF925120, BF925126, AA564576, BE159227, AC009466.17, AP002853.3, AP000880, 4.
HAGAN21	21	102695	1 - 829	15 - 843	Z69655.1, AL391987.15, AC004841. 2.
HAGBZ81	22	456414	1 - 1368	15 - 1382	AL532808, BF356940, T26989, F07451, T26988, BE089554, AV753931, AA176259, Z38391,
					AI652752, AU123074, AU132666, AV753734, BE876059, BF911695, AV755178, D61463, AI267311,
					AW387165, AW178928, AW374679, AW374832, BE089568, AW374731, BF700420, BF914304,
					BE173287, AW178920, AW751520, N83868, AW387129, BG170148, AW374762, AL120973,
					BE933886, AI915992, BE004012, AF224469.1, AF306765.1, AF184241.1, U03109.1, AF289489.1,
					583325.1, AF224468. 1.
HAGDG59	23	534165	1 - 1/20	15 - 1734	AV694248, BE895909, BE903848, BG02/942, AV651246, BG109861, BF240140, BF217326, BF669125, BE779936, AV650099, BF971092, AW875350, AW956342, BF107182, BF697022.
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	15 - 1280	15 - 742	15 - 1472	15 - 635
	1 - 1266	1 - 728	1 - 1458	1 - 621
	587261	022669	135227 8	587601
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	HAPNY86	HAPNY94	HAPPW30	HAPQT22

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HATBR65	64	635514	1 - 798	15 - 812	AW754098, AV747079, AW964560, BF827304, AI697254, AA826321, AA663880, BF924786, AA772037, AV725414, AA826164, AA663006, AA826322, BE062047, AA835931, AA319870, R95053, AV760830, BF918713, BF959165, AI053538, BF930653, BE828744, AA078591, AA139870, RA491430, AA078183, AW75205403, AW752051, AW752051, BF97813, BF95063, AV75011, AW973003, AA047821, BF93097, AA491430, AA078213, AW7520520, BF757569, AA077448, BG004304, AW793003, AA047821, BF932909, AA7076631, AW857010, BE183669, BE183617, BE699552, AV720211, AW973541, BE932909, AL254770, AL28454, AL251203, A124953, AV743864, AI251284, AW273541, BE932909, AL25473, AR95623, AV743864, AI251284, AW276578, AW7520729, BF952747, AA015737, AW975623, BF129140, AA076784, AA604863, BC722875, AV720104, BF952747, AA015737, AW975623, BF129140, AA076784, AA604863, BC722875, AV720104, BF9581982, A4519419, AA503018, AA503018, AA610881, AA503018, AA5004811, AA610381, AA503018, AA747757, H04977, AA604211, A1912401, AL27444, AC0044801, AC0044802, AC00448182, AC0049812, AC0050112, AC0052364, AP0003350.1, AC0050982, AC0044771, AC002106.1, Z9884.11, AF168787.1, AL157791.4, AC005198.1, AC003498.1, AC003408.1, AC003107.1, AC002106.1, Z9884.11, AF168787.1, AL157791.4, AL03495.13, AL162424.20, AC002107.1, AC002106.1, Z9884.11, AF168787.1, AL157791.4, AL03495.13, AC003589.2, AC00407706.1, AL162426.20, AL199317.5, AL399838.26, AL031005.1, AL109825.23, AC0049638.2, AC004477.1, AC0003992.4, AP000963.2, AC003690.1, US5740.1, AL139316.5, AC003690.1, AL5931382, AC004477.1, AC0003992, AP000963.2, AC0724028.10, AL034353.12, AC003503.1, AL5931382, AC004477.1, AC00099294, AP000963.2, AC0724028.10, AL034353.12, AC003503.1, AL5931382, AC004477.1, AC0009392.1, AL139317.5, AL39894.10, AL339318.2, AC003408.1, AL39318.2, AC003408.2, AC003408.2, AC003392.1, AL139311.2, AC003590.1, AL39313.2, AC003408.2, AC003392.1, AL139316.2, AC003690.1, AL393138.2, AC003408.1, AC00330.1, AL393138.2, AC004471.1, AC008392.1, AL139310.2, AP009363.2, AP009360.2, AP009360.1, AC00350.1, AC00330.1, AC00330.1, AC00330.1, AC00330.1, A

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HATCP77	51	748244	1 - 2084	15 - 2098	AI791525, AI733035, BF434939, BF433029, AI457816, BF478158, AI299145, AA910198, AA952936, AI301175, BF446488, AA904191, BF477842, AF209747.1, AF099137. 1.
HATEE46	52	565618	1 - 1661	15 - 1675	BE739761, BE867642, BG252738, BF670373, AI590088, AA452296, AW188012, AI467834, BF110214, AI698059, BE535889, BE220673, AI076779, BG170578, AW304047, AI653610, AW070709, AA015580, BE300577, AA705209, AI458930, AW173124, BG149183, AI037932, BF671524, AI597851, BE671575, AI310753, AI051897, AI128681, BF447913, AW295982, BF433016, AI300950, AI140885, AW473730, BF448227, N35880, AW770729, BF108371, R72042, AW302140, AA479329, AW023183, AA040787, AI494017, H98707, AI453020, AI932397, AA041222, AI038152, AA478593, AI459059, AA151356, AI168123, AI160559, AI125997, AI702632, AI073784, H97885, AV746537, AI433746, AI348429, AI025926, AW178814, AA035147, AI917957, N26242, AI189919, AI298395, AA225891, AI383747, AW085003, BF431762, AW079138, AI214632, H57061, N27692, W20186, AI537044, AI796916, AA661665, AI290329, AI38748, T39342, H99889, AA045554, BF433765, AI948963, AI143362, BE044374, AA767678, N36000, AI203768, H88073, AA311260, N91032, AW794932, N27062, AI382971, R19439, AI037915, AA825174, N26773, BE536609, AM192385, AW166934, AI979183, AA664910, AA056938, R20449, N92329, AI651355, BF942458, AW665523, BE046513, AA897347, AI829594, BF130347, BE814523, BF089510, BE738984,

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HBAFJ33	53	625916	1 - 1266	15 - 1280	AL134941, Al936102, AA806752, Al922844, BE396072, Al568741, AW593236, AW152304,
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					AA975643, AI032624, AI457317, BE858317, AA733170, AI334944, AI151526, AA478034, BF195105,
					AI291127, AI690771, AI220431, AL043583, AA593974, BE795539, AI096520, BG251676, AI094885,
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HBINS58	62	135238 6	1 - 829	15 - 843	AI827239, AW104045, AL536345, AL096774. 9.
HBJFU48	63	460392	1 - 835	15 - 849	BF674706, AA657543, AV757289, BE139139, AI250552, AI251284, AI251203, AI284543, AI251034, AW674277, AI25470, AW303098, AA582073, AI249853, AC005696.1, AF045555.1, AC090514.1, AF243527.1, AP001725.1, U91318.1, AL121897.32, AP003357.2, AC008155.9, AC005081.3, AL132838.4, AC011470.5, AP000692.1, AL132640.4, AL109976.23, AL121992.24, AL135928.6, AL033529.25, AL353807.18, AC020916.7, AL138849.12, AC011247.10, AL158830.17, AP000501.1, AC005521.3, AC011464.5, U95742.1, AC022384.4, AC011555.5, AL049795.20, AL033383.26, AC005921.3, AC012170.6, AC004922.2, AC007934.7, AC018828.3, AL121653.2, AL135783.6, AC044797.5, AP000355.1, AL121928.13, AE0066462.1, AL590682.9, AL451083.5, AL162724.16, AC004906.3, AC006312.8, AL359272.9, AP001666.1, AP001716.1, AF111169. 2.
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-	AI499131, AI5542	AI499131, AI554245, AI857296, AW002342, AI224992, AI573032, AW999049, BF817926, BE018711,
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	AF090900.1, AL13	AF090900.1, AL133640.1, AL050149.1, BC008387.1, AB063070.1, AL133016.1, AL162083.1,
	AL359596.1, AF09	AL359596.1, AF090896.1, AF146568.1, AL512733.1, AL136787.1, AK027868.1, BC008488.1,
	S78214.1, AB0553	S78214.1, AB055303.1, AK026045.1, AL442072.1, AF090901.1, AL136892.1, BC008417.1,
	BC007021.1, AB05	BC007021.1, AB055366.1, AL133557.1, AF104032.1, AF219137.1, AL442082.1, U42766.1,
.,	AK026855.1, BC00	AK026855.1, BC008365.1, AL117457.1, AL359618.1, AL049938.1, AB049758.1, BC003687.1,
	AF090943.1, AL04	AF090943.1, AL049314.1, AL136789.1, AJ242859.1, AF106862.1, AL137459.1, AF125949.1,
	AL136586.1, AB05	AL136586.1, AB056768.1, BC003683.1, AL389978.1, AL110196.1, AL136749.1, AL080060.1,
	AB048953.1, AF21	AB048953.1, AF218014.1, AK000212.1, AF111847.1, AF078844.1, AL122093.1, AL133080.1,
	AB063008.1, AB0	AB063008.1, AB047615.1, AL050116.1, AL050108.1, AL050393.1, AB055361.1, AF091084.1,
	AL162006.1, AL11	AL162006.1, AL110221.1, AL096744.1, AL050146.1, AL157431.1, AB052191.1, AL133606.1,
	BC006807.1, AB06	BC006807.1, AB063046.1, AL136799.1, AL137527.1, AL122050.1, AK026741.1, AB047801.1,
	AK027096.1, AF09	AK027096.1, AF097996.1, AK025339.1, AK026647.1, AL390167.1, AB060887.1, AK026452.1,
	AK026865.1, AK0	AK026865.1, AK026608.1, AK025958.1, AL359601.1, AK000323.1, AB048964.1, AL133075.1,
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	AL137283.1, AL51	AL137283.1, AL512719.1, AB060916.1, BC001045.1, AK000618.1, BC004556.1, AL122121.1,
	AK026533.1, AL13	AK026533.1, AL133093.1, AL512746.1, AK000083.1, AL050024.1, AK026744.1, AL389982.1,
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	AK025414.1, AB0	AK025414.1, AB060908.1, AL133565.1, BC006195.1, AB055368.1, AK026086.1, AL137557.1,
	AB060912.1, AK00	AB060912.1, AK000445.1, AK000432.1, AL049430.1, AF177336.1, AL136844.1, AK025092.1,
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	AL512689.1, AL12	AL512689.1, AL122123.1, AK027113.1, AB060826.1, BC008485.1, AB052200.1, AK025484.1,
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	AK025491.1, AK0	AK025491.1, AK026927.1, AB055315.1, AL136928.1, AK026532.1, AK026592.1, AL110225.1,
	BC008899.1, AB06	BC008899.1, AB060852.1, AL353940.1, BC006412.1, AK026959.1, BC002839.1, AL049382.1,
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НВЛСО1	65	638410	1 - 858	15 - 872	AW962384, AW956292, AA631830, AV708590, AW964544, AV709418, AI814702, AV729132, AV726091, AA652816, AV657453, AW956077, AW962908, AW966634, AW966349, AV708167, AV7026091, AA652816, AV657453, AW956077, AW962908, AW966634, AW961606, AW960832, AV703597, AV727065, AV70338, AV703232, AW961903, AV70331, AI525316, AV703761, AV729517, AV726754, AV707276, AW961313, AW963348, AV705525, AW962942, AW963383, AV966270, AV708720, H60864, AW950748, AC004033.3, AC007050.25, AC008745.6, AC005500.2, AC008265.15, AL590763.1, AL359235.3, AP000789.4, AC005476.4, AC079602.15, AC009789.21, AC018638.5, AC024952.4, AL022318. 2.
HBJLF01	99	732111	1 - 1918	15 - 1932	BG261130, BG121213, BF347966, BF796462, BE899286, R17115, A1123525, A1697325, BE783654, AW402585, AA032055, BF724098, AA031919, AW402594, AW402872, AW026287, W89010, A1926967, W95778, BF887406, A1376419, BF38132, BF507805, BF888120, AA233002, A1669291, A1963299, BF744292, BF907549, BF907541, A4954836, BF888127, A1768850, AA768759, BF888128, AA232951, BF744299, AW090314, A1571824, BF888074, N73038, AA480645, N53675, AA886377, BF888119, AA535561, A1864506, BF799491, A1217778, N51612, BF381336, N53906, BE819619, A1806785, BF744934, W95735, BG251027, BF381311, A1674508, AA016130, AA743705, AA917873, AA649797, BF887394, AA631017, BF907590, A1480218, AW302053, BE139664, Z39059, H86222, AA9554334, AA456896, A1244571, AA015836, A1341715, AA485019, A1078627, A1015866, AA827439, BF745018, AW271993, AA954612, AW001670, AK000208.1, AC011005.7, AC083866, 2.
нВлгн40	19	828130	1 - 1839	15 - 1853	AA830583, AA465482, AA731000, AA815064, AI632903, AW576518, AA847860, W84413, AA210914, AW341113, AA721650, AA488009, R45299, AW873717, AI693003, AW977787, AI283768, AI127928, AI148391, BE048487, AA417947, AA236463, AI671420, AA836581, Z38691, AA811097, AW471001, AA210913, AI500017, AA709242, AA418189, AI492414, AA234646, AW956166, AV703593, AW950675, AW963117, AV706278, AV701983, AW954129, AW965551, AC013414.7, AK026400. 1.
HBJNC59	89	112580	1 - 1047	15 - 1061	AW007501, AA902287, AI858092, AI005351, AW959933, BF342564, AW083940, BF820646, AI870864, AW960414, AI032697, AW149115, AA829811, AA709070, AW264612, AA643392, AI951841, AA614344, AI312642, AA533443, BF850030, AI799536, AA991955, BG222284, AI830766, AA594172, AI289881, AI741805, AI276207, AW088660, AW268666, AI749660, AI369678, AI264768,

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	A1866469, BG032036, BF792099, AL515375, AL514829, A1568060, A1540606, AA830839, A1678446,
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	ALU301/0.1, AF230496.1, BC000530.1, AF132/30.1, AF0615/3.2, ALU800/4.1, AF218031.1,
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HBNAW17	69	668268	1 - 906	15 - 920	AP002088.2, AC007429.11, AC020612.40, AL513015. 6. AA713518. AA807610, AW104604, AA830415. AW975518. AL138824. 19.
HBOEG11	12	130075	1 - 1342	15 - 1356	BF056642, BF516162, AI807970, AI081658, AA861514, AI494148, AW448950, AI973060, AI400318, BF849398, AA385680, AW028539, BF847907, AA377456, F34025, AI472684, C01967, BF344191,
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HBOEG69	72	793786	1 - 1397	15 - 1411	AW576190, AA524064, BF701378, AI337569, AW058654, AW964434, BE568412, AW978965, AW241842, BE221243, AI346249, AW241843, AA825846, AA936562, AI184881, AI346396, AA570030, AW368546, AA465472, AW995507, AW361365, AV743550, W74158, AV750714, H80936, BF879997, BF880246, AI144077, AV743963, AV740879, AI053597, AI222773, R95913, BF901243, AA318779, BF088361, D62291, R27740, BF767423, AI277044, AV743740, AI053934, AI310256, R27741, R08998, C00592, N64904, AA827757, AK024978.1, AC006146.2, AF147723. 1.
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	15 - 728	15 - 986	15 - 4893	15 - 1410
	1 - 714	1 - 972	1 - 4879	1 - 1396
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	124	125	126	127
	HDPH151	HDPJF37	HDPMM88	HDPNC61

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	1-1713	1 - 2490
	897276	683371
	128	130
	HDPOE32	НДРОН06

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1 - 1891	1 - 3077	1 - 1382
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HE2PD49 157	638617	17 1 - 1408	15 - 1422	
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237	238	239	240	241
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ННҒНЈ59	246	411332	1 - 647	15 - 661	AA833770, AW877426, AA804902.
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	15 -	15 -	15-
	1 - 697	1 - 861	1 - 876
	662329	544615	579890
	250	251	252
	нндсм76	ННGСQ54	HHGDF16

HHGDW43	253	554613	1 - 1036	15 - 1050	AV701584, AV726913, AV704346, AV728464, AV707827, AV693230, AV687808, AV705939, AV708600, AV705045, AV704029, AV702601, AV655568, AV727449, AV701067, AV727266, AV705517, AV650430, AV704588, AV702830, AV702086, AV728521, AV725260, AW951773, AV726646, AV703833, AV705813, AV729463, AV70544, AV703653, AV726903, AV725970, AV707500, AV728256, AL1334184, AK023144.1, AF214114.2, AF208045.1, AF227899. 1. AU122180, BE070260, BE070199, N47096, AA633840, N50530, N49396, W00508, AC079353.5,
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HLWCF05	327	460619	1 - 632	15 - 646	AW673972, AA524980, AI961840, AW515257, AA877458, AI336752, AW070880, N66443, AA528268, AI273991, N26777, AA004802, BF990906, AA700372, AI290414, AA906772, AI243008, H17960, AA502507, AA860313, AW470183, H84037, BF348530, R54094, BF764578, H84462, R30859, BF764695, AI864306, AW022917, AW970612, D45536, AI908718, BF878700, AW999226, BC003414.1, AL450487.17, AK025020. 1.
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HMDAE65	338	520338	1 - 684	15 - 698	AL035447.6.
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нмеет96	343	566720	1 - 1323	15 - 1337	AL521371, BF337502, BG249151, BG113640, BG260630, AL521372, AL516032, AV731587, BE384522, BE973743, A1735261, BE563906, BE277846, A1808277, BF667795, BF691333, AW958349, BE871082, BF791366, BE58906, BE577846, A1808277, BF667795, BF691333, A1368797, BF572289, AA583057, BF664548, BE567499, AA807741, A1828551, W022860, A1088857, N44490, AW439214, A1026716, N73457, A1142511, N34764, AA633495, BF346426, AA594963, BG258660, AA862351, A1356184, AW518053, H98681, A1125040, A1306645, AW675383, A1280832, AV729211, AA748024, A1707840, AA830528, AA916426, A1285008, BF743169, AV724056, BE531141, H04537, T71560, T87237, BE855394, H29267, T71330, AW078897, AA507967, BF790198, AA613581, AA215785, H09795, AL516031, BE763380, T71482, A124966, A1783537, AW853901, T79791, AW853890, AA459511, T97835, D60812, AV711819, H04458, N27248, AA483615, BE615442, A1685127, BE616237, F10230, BF239125, H94779, BE093345, AW168908, BF541751, T74091, H09880, H29351, BE833069, T82010, AA082465, AW951663, A1919531, F12612, AA452714, AW068971, BE697991, AA450068, AW024907.
HMIAL37	344	603201	1 - 1406	15 - 1420	AW934844, AL045824, AI269960, AW300030, AA860926, AI761354, AI739238, AW351654, AI984995, AW390711, BF931410, BE464037, BF229829, BE764327, AI628985, AI989344, AW013904, AI869919, AA121174, AI453367, AI270726, AI272081, AI869907, W22160, AW192301, BE463416, AI991419, AI796741, AA551799, AI738967, AI738958, AI783811, AW304132, AA344913, BF229794, BF798430, AW843500, AW88833, BF798442, BE763828, BF761128, AA121198, BF333846, BF928080, AW062449, AA327309, BF800375, BF800393, AW845326, BF808207, BF819298, AB018687.1, AB006955.1, AF039700.1, AF039699.1, AC005137. 1.
HMIAP86	345	726831	1 - 1660	15 - 1674	AL533220, BF967956, AL533253, AL520510, BE735407, BF972030, BE735149, BE615619, BE616472, AI873527, BF347687, BE383692, BF967233, BE385645, AW593348, AW381588, BE616472, AI873527, BF347687, BE383692, BF967233, BE385645, AW593348, AW381588, BF541528, AI032869, BE294015, AA404241, AI564151, BE294088, AA401224, AI682367, BF694848, BE555192, AA910774, AI367739, AW976142, BE615232, BE389860, BF029472, BE615138, BE645680, AI131262, AA054608, AI479085, BF728074, BF672705, AI241428, AA021119, AA142931, BG108596, AI039086, BF348256, AV748480, AA021118, AA056945, N48177, AI202193, AI491859, N53324, AI364707, R44688, AA015735, AW015622, AA905989, AA813639, AA057005, AA035652, AA917010, AI952221, AA054548, AA015832, AA505774, AI697106, R19440, BE707409, BF841914, BE677828, AW954134, AW950006, AW954211, AI968179, AW960629, AW964070, AV728721, AV656478, AW953797, AV6869931, AV683994, AV703878, AV702019, AV705014, AV728733, AV727510, AV706741, AV726026, AW952460, AV709596, AV709273, AV725633,

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HMKCG09	346	548078	1 - 907	15 - 921	BE043082, AI927692, AW058564, AW055230, AW015122, BF592005, BF196476, AA814450, AI634533, AII39038, BF446797, AI277016, BE045365, AA732327, AI435146, AA290626, AA832487, AW964897, AV682305, W56110, AI796930, AI949631, R48833, AI800208, AI628443, BF431339, BF371245, AI935532, AI582596, AA319436, AA832489, T59460, AA806730, AA279760, AA325502, AI935529, C20681, T59406, AA766259, BF089238, AL035209. 1.
НММАН60	347	562776	1 - 808	15 - 822	AA736481, AI288032, AC004587.1, AC004031.1, AC002073.1, AC009137.6, AF001550.1, AL109628.5, AL121594.6, AL133215.16, AC024584.5, AC007688.15, AC005874.3, AF134471.1, AC002565.1, AC004678.1, AC003950.1, AC007546.5, AC002395.1, AC011529.3, AP002906.2, Z83826.12, AC009470.4, AC004703.1, AL050335.32, AL117354.12, AL136418.4, AL139054.1, AC005914.1, AL022313.1, AC002044.1, AC020633.3, AC018758.2, AC007779.4, AC013734.4, AC019205.4, AC005844.7, AL033519.42, AL162601.5, AC011484.4, AC020916.7, AF176815.1, AC007390.3, AC007371.16, AC009488.5, AL162615.13, AC002978.1, AC027319.5, AC01848.5, AC018476.8, AC055120.5, AL035422.12, AF031078.1, AL136218.26, AC008521.5, AC083871.2,
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	15 - 456	15 - 616 15 - 575 15 - 1144 15 - 703	15 - 1649
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	367	368 369 370 370	372
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	1 - 625	1 - 506	1-510	1 - 1021
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	373	374	375	376
	HNGBT31	HNGDG40	HNGDJ72	HNGDU40

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380	381	382	383	384	385	386	387
HNGIH43	HNGIJ31	HNGIQ46	HNGJE50	HNGJO57	HNGJP69	HNGJT54	HNGKN89

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	15 - 956	15 - 742	15 - 1298	15 - 905	15 - 762	15 - 725	15 - 606	15 - 793	15 - 426	15 - 843	15 - 2642	
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	836064	843515	892160	496115	520300	520294	520298	531908	410114	135220	985880	463568
	388	389	390	391	392	393				397		399
	HNGOM56	HNGOU56	HNGOW62	HNHAH01	HNHCX60	HNHCY64	HNHCY94	HNHDW38	HNHDW42	HNHED17	HNHE142	HNHF029

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		15 - 607	15 - 1355															
	1 - 1667	1 - 593	1 - 1341															
	646709	562728	843488		-													
	400	401	402															
	HNHFR04	HNHFU32	HNHOD46															

					AW517023, AA338985, AA033605, AA359435, AW247428, BE169006, BF108984, Al864722, AW247387, BF111419, AV704626, AW732331, AA825440, BE168970, AI983715, AW878738, BE302856, T24108, AI979211, AW992807, AW863091, AW878649, BE241911, AA852854, BG005253, AW271173, F26257, BE048939, AF104222.1, BC000495.1, BC001947.1, AC006529.1, AB033004. 1.
HNTCE26	406	5	1 - 2149	15 - 2163	BG252201, AV726464, AL529709, BE894106, AV726994, BF970560, BF132059, BF977798, AI703275, AW512938, BG164577, AL529708, AI767521, AI823746, BE220262, AA583438, AI143608, AW468337, AI949854, AV727138, AI620344, AI209187, AI630993, BG007081, AI004986, AI565892, AV715169, AI367983, BF056815, AW394003, R70620, BG007658, AA152183, BF381743, AA565300, AA088574, AA931697, AA995899, AI025252, AA297479, T84083, AW138535, H71679, Z45535, AA297478, AI865989, AA367654, AA150060, AA044326, AW338484, D29436, R24591, AI005551, H00983, H39751, AI669105, T83438, BF091777, AW138127, R21165, BF083909, BE934286, R76620, AA971307, AA745052, AW945769, AI554153, T84151, BE550213, H01724, AW051517, AW373316, AW373313, T89390, BF083903, BE541509, AA180271, AI263504, AF303588.1, AF140242.1, AL133390.7, AF056032. 1.
HNTNC20	407	700627	1 - 1965	15 - 1979	BG179496, BG254440, AA573206, A1735586, BE326906, AA131359, BF668303, AI522318, AI376670, AW241377, BE350501, AA452451, AA131240, AW242329, AI540415.
HNTNI01	408	135228 5	1 - 2073	15 - 2087	AA447485, AA196688, M86015, AI750365, R13985, BF356780, N28763, AC005028. 1.
HNTSY18	409	104138 3	1 - 1797	15 - 1811	AW470226, BF058886, AI692966, BF058139, BE218656, AI281699, AI241829, AA613450, AC004877.1, AL137162.25, AJ400879.1, AC011551. 3.
НОААС90	410	130120 2	1 - 628	15 - 642	BF508077.
HOACB38	114	520201	1 - 592	15 - 606	AU8813106, AC069262.24, AC007421.12, AL354735.14, AC004382.1, AC009131.6, AC090939.1, AP000359.1, Z86090.10, AP001748.1, AL049843.18, AL021391.2, AC015801.25, AL133243.1, AD000092.1, AJ003147.1, AF243527.1, AC004125.1, AC007991.7, AL035086.12, AP001724.1, AC006038.2, AL121886.22, AL133448.4, AC007981.46, AC005207.1, AL359853.18, AC002477.1, AF205588.1, AC013429.12, AL121809.6, AC004980.4, AJ229041.1, AC002430.1, AC001475.6, AC009123.6, AC008521.5, AC009506.5, AL139099.2, AF207550.1, AE000661.1, AC006141.2, AC001412.7, AC007899.3, AC005746.1, AP002360.4, AL359751.12, AC011811.42, AL158207.15, AC005332.1, AC02552.4, AC008569.6, AC007064.27, AL138752.5, AL049830.3, AC015971.4, AC026749.5, AC016637.6, AC08569.6, AC007064.27, AL138752.5, AL049830.3, AC015971.4, AL139316.5, AC018644.6, AC012170.6, U91323.1, AL121992.24, AF258545.2, AL1333370.4, AL020997.1, AL163201.2, AC008403.6, AC004816.1, AL168787.1, AC005522.2, AC027319.5, AL133357.4, AL139316.5, AL133316.5, AL1333316.5, AL13333674.5, AL1333316.5, A

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	15 - 1118	15 - 830	
	1 - 1104	1-816	
	835049	520348	
	412	414	
	HOCNF19	HODDN65	

HODDN92	415	422913	1 - 1925	15-1939	AL1371399, AF107885.2, AC068833.7, AP002085.1, AL136219.17, AL033529.25, AF254822.1, AC005793.1, AC004000.1, AC006480.3, AC008736.6, AL353701.15, AC004382.1, Z93015.9, AP001330.3, AC006312.8, AC005940.3, AC008736.6, AL353701.15, AC004382.1, Z93015.9, AP001303.3, AC006312.8, AL034420.16, AP001748.1, AC005915.2, AL034424.9, AC006512.12, AC001302.3, AC003312.1, AC01490.7, AL1180510.22, AL022069.1, AP000065.1, AP001752.1, AC004971.3, AC00372.1, AC0004971.3, AC00540.2, AC005082.2, AC003731.1, AC004871.3, AC00540.3, AC00372.1, AC006487.2, AC005642.2, AC005082.2, AC00372.1, AC004871.3, AC00540.2, AC005082.2, AC00372.1, AC004871.3, AC004871.3, AC00540.2, AC00372.1, AC004871.3, AC004871.3, AC00290.1, AC010519.6, AL163208.2, AC01388.5, AC01238.1, AC010519.6, AL163208.2, AC00577.5, AL137072.8, AC00806.4, AB038653.1, AC004491.1, AS33.1, AC01442.4, AC00625.2, AC01388.5, AC01238.1, AC01442.4, AC00625.2, AC01388.5, AC01238.1, AC01442.4, AC00625.2, AC01238.1, AC01442.1, AC00625.2, AC01472.1, AL138762.20, AL5234.1, AC006057.5, AC01338.1, AC01442.1, AL138762.2, AL13707.4, AC00625.1, AL13707.2, AL13707.4, AC00625.1, AL13707.2, AL13707.4, AC00625.1, AL13707.2, AL13707.4, AC00625.1, AL13707.2, AL13707.4, AC00625.1, AC00637.3, AC01338.1, AC004986.2, AC00141.1, AL086701.14, AL080701.11, AC004477.1, AL12702.0, AC00554.6, AL13708.1, AC00447.1, AL13708.2, AL13708.1, AC00447.1, AL13708.2, AL13708.2, AC00141.1, AL13708.2, AL13708.2, AC00141.1, AC00447.1, AL13708.2, AC00447.1, AL13708.2, AL13708.2, AC00441.1, AC00447.1, AL03468.2, AC001862.1, AC00562.1, AL13353.9, AC00441.1, AL035252.5, AP001610.1, AP002535.1, AC005560.1, AL13353.9, AC006449.19, AL035252.5, AP001610.1, AP002535.1, AC005560.1, AL13360.1, AL13809.16, AC00847.1, AL1980.1, AC00567.1, AL1336.0, AC00847.1, AC00847.1, AC00848.2, AC00846.1, AC00847.1, AC00847.1, AC00848.2, AC00846.1, AC00846.1, AC00847.1, AC00846.1, AC00846.1, AC00846.1, AC00846.1, AC0084.1, AC00846.1, AC0
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HODDO08	416	790333	1 - 1762	15 - 1776	BF037067, BF690178, BF037467, BF690717, BE613160, BE262757, BF690612, AA878758,

AA863301, BF897824, AA401453, 5, AI093151, AA099024, AA699676, AI911997, AI924160, BF815573, BF897801, AI806115, AI261776, AI310423, BF940128, ILAW026697, AW197588, AW338979, ILG54526, BF477527, BE964777, AW628128, AI147095, AA070339, AA693726, D, AI085327, AA132700, AW268656, A780169, H73783, AA292088, AA693704, BF964464, AA132811, BE620176, IE567691, AI192239, AW247578, AI289150, H091, AI948639, AA863079, W24068, 932, BF573651, BG057973, AI283354, 66, AA363605, BF691459, BF038622, A011640, AI452472, AA070149, H96713, 4303985, AW149938, AA405427, 823, AA379017, AA346687, BF809804, I, R05554, D80913, AW884514, AW166740, 80412, BF798512, R22581, AA046773, 2, BE313283, BE962739, AW999933, 324, AC007782.20, AC025594.5, L096791.12, AL137786.2, AC006449.19,	Total Control of the			, AV707090, BF892766, AA528261, 86.4, AL512449.6, AL360179.8, 2361.10, AL133373.5, AC027287.20, AL138758.7, AC034240.4, AL121575.24,	AL 157827 17 AB011792 1	, BF815287, BE300677, AW239056, AI783820, AA362844, AW795506,
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	15 - 682	15 - 739	15 - 1126	15 - 851	15 - 747	15 - 2520
	1 - 668	1 - 725	1 - 1112	1 - 837	1 _ 733	1 - 2506
	579256	835027	119486	834907	768375	828177
	417	418	419	420	421	422
	HODDW40	HODEJ32	HODFN71	HODGE68	HOFRK34	HOEBZ89

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НОЕDB32	423	634994	1 - 1448	15 - 1462	BE220144, BF25463, AL043598, BE379024, BE729709, BE388931, BF058202, BE389160, BE218910, AA937045, BE888648, BF983681, BF058514, BE729777, BE386542, BE270287, BF219910, AA937045, BE888648, BF983683, BF058514, BE729777, BE386542, BE270287, BF219910, AA937045, BE88648, BF983683, A1806995, BE302761, A1218926, A1040017, AV700992, BF204637, AW269653, AW664365, BF851636, AA558441, A1971923, BE389935, A1971822, A1984087, BF109553, BE149505, A1371806, BE466285, N63999, A1218921, BE896831, AW105333, AW264122, H97490, BF830445, AW410288, AW856197, A1041603, AW469216, N28797, BE379424, AW662759, A1218000, A1283819, AA789225, AA916425, W67366, A1354311, AW517796, A134922, AA872912, BE207555, AW410287, A1751344, A1537028, AW379887, A1469495, N23215, AA305895, AV700226, A1399649, AW602751, A1857609, BF832669, BF738545, BF732356, AW960917, W67367, A1093054, AW132083, AA613324, A1220983, AW241183, AJ239424, AW876666, N32087, A1126987, AA166810, A1751345, T58592, R57961, BF929058, A1015141, AA3751135, C01839, H14764, AA4885934, AA359174, A1280938, D18283, BF512261, BC000526.1, AL117619.1, AF132000.1, AC003687.1, AL049873.3, AL450324. 10.
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	15 - 2794	15 - 2048	15 - 2406
	1 - 2780	1 - 2034	1 - 2392
also to delicate the second of	135237 8	847424	847425
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	HOFNC14	HOFND85	HOFNY91

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	446	744	448
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	449	450	451	452	453
	HOUDK26	HOVCA92	HPASA81	HPBCU51	HPDDC77

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	1 - 2634	1 - 3093
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	15 - 1466	15 - 566	15 - 1274	15 - 1217	15 - 1656	15 - 2543
	1 - 1452	1 - 552	1 - 1260	1 - 1203	1 - 1642	1-2529
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15 - 1461	15 - 559
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471	472
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	15 - 1941	15 - 1510	15 - 805	<u> </u>			15 - 1182	15 - 600	15 - 777					
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HSAYB43	HSAYM40	HSDAJ46	HSDEK49

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HSDER95	498	664502	1 - 560	15 - 574	BE881136, AW005333, AA631227, AA143192, AV707034, AA181022, AI301959, H98648, BF507561, AU143221, BF514388, AA594850, AI478582, AV681894, AA287457, AI393857, N75788, BE044258, AA211849, F06608, N22567, AW450628, AA563681, AW195766, AI915322, BF701252, AA186657, AA992992, AA143136, AI302352, BF035111, AA631048, AV706818, AI341927, AV703142, BF446906, BE693540, AW961036, BE676990, AI870902, AV744251, AV749732, N75929, AW887695, AA973384, AA160641, AA338837, AK024037.1, AL359596. 1.
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HSDFW45	200	589974	1 - 1728	15 - 1742	AA235952, AA235753, H40529, AA297145, BE139139, A1250552, BE062159, A1251034, AW970571, A1284543, A1251284, AW664460, BE138387, AW968338, AW023111, AA562991, AV655282, A1355559, BG059314, A1254700, H91062, A12446623, BE000614, AW276678, BF131490, A1551529, BG059314, A1524700, H91062, AA746823, BG060614, AW276678, BF131490, A155145, T74524, BF917346, A1278471, BF968874, AW328000, A1281561, AA642809, AA515048, A1821764, A1732445, N55315, T74524, BF917346, A1279417, BF968874, AW328000, A1281561, AA642809, A151464, A1732483, AA665960, AW237905, AV761107, T50676, A1066646, AL524675, BF030962, AC010000.5, AL392166.19, AC007546.5, AP0007194, AC011811.42, AC0240831.3, AC010427, AC007546.3, AC0072772, AC002777, AC003805.1, AC0084938.2, AL445483.13, AC010427, AC007263.4, AL390298.13, AC010427, AC008491.6, AC0114504, AC011479.6, AC011469, AC012627.4, AL035251.11, AC008805.7, AC084991.6, AC010465.4, AP001779.1, AL158207.15, AC008895.7, AC004438.1, AL245483.13, AC0042439.7, AC001465.4, AP001779.1, AL158207.15, AC008895.7, AC006435.1, AL245483.13, AC006435.7, AC006349.8, AC011469.6, AL365805.15, AL13776.1, AC008895.7, AL13878.10, AL353716.18, AE28874.1, AL390241.19, L78810.1, AL109936.10, AC007656.2, AL137574, AC005806.1, AC007681.3, AC006435.7, AC008893.3, AC005401.3, AL137598.1, AL137978.1, AL137978.1, AL13736.2, AL354696.11, AC00865.6, AC002378.1, AC006181.3, AC01618.1, AC0089936.10, AC007656.2, AL1372991.1, AL13785.5, AL137878.3, AL135260.1, AC08655.6, AC002378.1, AC00611.13, AC006940.3, AE241728.1, AC006098.6, AL049843.1, AC069945.2, AC002098.6, AL049880.3, AC017079.5, AL35498.1, AC08995.1, AL355498.1, AC017079.5, AL35466.1, AL35469.1, AC01709.2, AL454891.0, AC01709.2, AL35469.1, AC069944, AL137792.11, Z99941.1, AC01146.5, AL13546.1, AC069941.2, AC01503.2, AL35469.1, AC01503.2, AL35461.1, AC01693.1, AC01693.1, AC01693.1, AC01693.1, AC01693.1, AC01693.1, AC01

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HSDJM31	504	491112	1 - 547	15 - 561	AA426010, AI986451, BE856226, AA773781, AI699994, BF477477, BF929123, BF526671, BF341281, AW020695, BF929118, BF966870, BF966816, BF966822, BF342126, AV726843, AC018616. 5.
HSDSB09	505	130149 8	1 - 795	15 - 809	BF432333, AI861851, AI240993, AI795956, AI074484, AI640759, AW006868, AW241621, BF592070, AW271387, AW614840, AW450466, AW243423, AI244694, AI640517, BF431431, BF431530, AI439169, AI613108, AI915938, AI984796, AI245393, AW300335, AA931466, AW235983, AC005722. 1.
HSDSE75	206	545057	1 - 1137	15 - 1151	AW378251, BF349814, AA687791, BF739001, AW378183, AA661723, H61383, T88677, H62404, AA443169, AW339864, AA458622, AA252063, AI129690, AW960791, AB006755.1, AB006756.1, AB006757. 1.
HSDZR57	507	651375	1 - 294	15 - 308	BE255995, AW473473, AW206723, BE312252, AI571368, AI810895, AI479711, AI656582, BE676619, AI492370, AI929750, AI762058, AW271956, BF591321, BF434884, AI500262, AW612319, AW085870, AI627969, AW168428, BE796769, AI767097, AI205848, AA632229, AI565786, BG033526, AV729047, AA876257, BE563237, BE905450, AA478285, BE257238, BE878838, BF664024, AA641693, AA478343, BC002907.1, AK000519.1, AC008755. 6.
HSHAX21	208	612823	1 - 1972	15 - 1986	BE379784, AL522216, AL520172, BF439334, Al652855, Al766309, BF512139, Al635715, AW299533, AW299897, Al129966, AW411210, Al624534, Al925109, Al803484, Al804159, BF184613, AA279212, Al609083, Al969459, Al860837, AA879465, Al183591, AW104990, AW316983, AW474646, AW630619, Al955714, AW409582, AA678827, BE139077, AA766602, Al431314, BF087963, AA081236, AW194027, BF701425, Al521521, AA588351, Al923638, AU155980, N39554, AV686756, AA769352, R78080, AW613876, AA259257, R22218, AA443811, AA969814, AA729654, R80114, T60532, Al969030, AW572611, AA259256, R80005, AW805183, BF592136, T51990, BE972627, Z38832, R23587, R24524, T52102, AA371263, Al564179, Al783565, BF700820, BE619819, AA447188, AK001845.1, AL136705. 1.
HSIAS17	509	135219	1 - 1767	15 - 1781	AL519037, AL522565, AL519036, AL529136, AL529135, AL530266, BE745103, BF528553, BF991144, BE745909, AW328641, BF796812, AL523650, AL525532, BE889377, BE514827, BF981144, BE745909, AW328641, BF796812, AL523650, AL525532, BE889377, BE514827, BF982724, BF036473, AW241827, BE378558, BE207101, BE675053, AI888192, AI990765, AW583031, AA469984, AA469998, AI660851, AW615511, AA412213, AW269957, BF589410, AA233023, AI339908, AW183546, AI434667, BE300850, AA834131, AW004730, AW138531, AA233023, AI339908, AW183546, AW138564, AA232705, AI698753, AA340084, AW584027, AI950847, R09010, BE151689, AI864316, AA523207, R05695, BE1227646, BE122728, AL045891, AL041862, AL042898, AL079977, AL047092, AL047163, AL046356, AL043089, AL043321, AL043196, AW858522, BF726868, AL042745, AL042488, BE047737, AW772685, BF726504,

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	BE874133, AW673679, AL045163, BG252040, AI923509, AL514843, BG105240, BE875243,	
	BG168185, AL514939, AL042628, AI494201, BE963560, BE048081, AL047611, AV729953,	
	BE910373, AL514219, AL040243, BG110517, AL042365, AL049085, AI432644, AL515225,	
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	AW151136, AL514773, AI539771, BF814504, AI620284, BE785868, BF726207, AI364788, AI537677,	
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	BE061378, BE965121, BE672647, AL121270, A1076519, A1874166, A1889147, A1382932, A1284517,	
	AISUU/U0, AI443231, AI491//0, AW131136, AI669169, AI321300, AI3200002, AI264309, AI336663, Ai666168 AI6661730	
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15 - 1466	15 - 1019	15 - 973	15 - 1430	15 - 1949
1 - 1452	1 - 1005	1 - 959	1 - 1416	1 - 1935
560744	526021	532001	838160	8 8 8
581	582	583	584	288
HTOAK16	HTODK73	HTODO72	HTOGR42	HTОНМ15

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	15 - 1499	15 - 1558	15 - 549	15 - 1294		
,	1 - 1485	1 - 1544	1 - 535	1 - 1280		
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	586	287	588	288		
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AI561060, AW872575, AW268300, AW576391, AI341664, AW438643, AV764398, AV729809,
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	HWADJ89	HWBAO62

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BF690640, BF576363, AW813018, BF699331, AV714362, BF978687, BE866124, BF672111, BF670420, BE866568, AV755701, A1814859, BF665931, N92494, A1829932, BF698791, BF671127, W021913, BF671702, BF982689, BF184136, BF67326, W2978, AV681672, A1522384, AV753993, BF104739, AA102746, AW581807, AW390508, BF69725, W397728, AV681672, A1523284, AV753993, BF104739, AA102776, AW390508, BE87326, BF242452, AV712182, BE891500, BF216657, BF681132, BF671182, AV716096, BE873981, AV73346, AW444946, BF971829, BF691500, BF21846, C05938, AL524593, BF24326, BF031857, BF691267, BF691257, BF691257, BF691257, BF691257, BF691257, BF691307, C17464, AV753085, AV3069344, BE858177, BF213466, C05938, AL524593, BF573310, AW338919, AV712127, AV755085, AA309029, BF694056, A18840386, BF693807, C17464, AV759457, A1934573, BF214152, AA071179, BR810215, BF693807, C14373, BF673387, BF694056, A185029, BF694056, A18840385, BF131605, A1142543, BF757533, BF73716, BF774652, AA143582, BF106013, A1124903, AW162310, BF676442, BE855418, AA608786, BF233036, D59738, AL119812, BE874244, BF692570, AA430087, AW160345, BF693361, BF77781, A1374863, A113742, BG010683, BF693336, BE493250, AA4308702, AA059864, AA569765, A1143310, AA658303, A1360862, A1277781, A1374863, A11374863, A1137483, A1157832, BF574336, BF603736, BF603056, BF603059, BF603059, BF603059, BF603059, BF603059, BF603056, BF603059, BF603059, BF603079, AA846371, AA53448, BF574320, AA016495, BF6000793, AA028916, BE939314, AV755293, BF738002, AA446457, AA446433, AV734138, AW401449, BF907020, AA846371, AA15828, AB167730, AA846371, AA1582, BF600793, AA628916, BF60703, AA64643, AA77844, BF71477, A1032001, BF368911, A1057310, AW149028, AW836319, D80244, A1077911, AA14588, AA390929, BF382245, AI640870, A1934317, AA810465, BF239551, AA835669, C18148, N20411, BE86610, H00317, H00365, H05990, H25943, H2943, H49423, H48481, H29738, AA8333, R78460, H00317, H00365, H05990, H25943, H2957, AA06872, AA06872, AA06873, AA0833, R82460, H00317, H00368, AA06872, AA06872, AA06873, AA0833, R8333, R83436, H003693, AA0832, AA0832, AA0	218 AA677440, AW994068, AA368613, AW052024, AI633325, AA865554, AA011059, AA011060, AW955888, AU156208, BE177677, AF198488.1, AL137740. 1.	
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•	AW872575, AI610376, AA629572, AL041690, BE967369, AV764398, AW970848, AA720702,
	AU145393, BF919090, AV757607, AI287651, AA613345, BF984160, AI432270, AI890918, AV750172, AE074677, AV730001, BE680630, AV764530, AW076475, AI718446, AW120001
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	BG036337, AI568678, AW407578, AW472872, AV760937, BF965007, AI379719, AW265009,
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	AC012003.9, AC011484.4, AC002565.1, AL021154.1, AJ010598.1, AL161656.20, AP001717.1,
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## **Description of Table 4**

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Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1B.2, column 5. Column 1 of Table 4 provides the tissue/cell source identifier code disclosed in Table 1B.2, Column 5. Columns 2-5 provide a description of the tissue or cell source. Note that "Description" and "Tissue" sources (i.e. columns 2 and 3) having the prefix "a_" indicates organs, tissues, or cells derived from "adult" sources. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease." The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector use d to generate the library.

AR054	Donor II Resting B Cells	Donor II Resting B Cells	<del></del>
AR055	Heart	Heart	_
AR056	Human Lung (clonetech)	Human Lung (clonetech)	-
AR057	Human Mammary	Human Mammary	
050	(Ciolificali)	Uman Thomas	т
AKU38	(clonetech)	(clonetech)	т
AR059	Jurkat (unstimulated)	Jurkat (unstimulated)	
AR060	Kidney	Kidney	
AR061	Liver	Liver	
AR062	Liver (Clontech)	Liver (Clontech)	Т
AR063	Lymphocytes chronic	Lymphocytes chronic	
	lymphocytic leukaemia	lymphocytic leukaemia	$\neg$
AR064	Lymphocytes diffuse	Lymphocytes diffuse large	
	large B cell lymphoma	B cell lymphoma	$\neg$
AR065	Lymphocytes follicular	Lymphocytes follicular	
	lymphoma	lymphoma	T
<b>AR066</b>	normal breast	normal breast	
AR067	Normal Ovarian	Normal Ovarian	
	(4004901)	(4004901)	7
AR068	Normal Ovary 9508G045	Normal Ovary 9508G045	Т
AR069	Normal Ovary 9701G208	Normal Ovary 9701G208	T
AR070	Normal Ovary 9806G005	Normal Ovary 9806G005	$\neg \tau$
AR071	Ovarian Cancer	Ovarian Cancer	
AR072	Ovarian Cancer	Ovarian Cancer	
A D 0.72	Overior Concer	Overien Center	Γ
C/02	(9707G029)	(9707G029)	$\neg$
AR074	Ovarian Cancer	Ovarian Cancer	
	(9804G011)	(9804G011)	П
AR075	Ovarian Cancer	Ovarian Cancer	
100		(9000013)	Т
AK0/6	Ovarian Cancer	Ovarian Cancer	٦

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(9807G017)	Ovarian Cancer (9809G001)	ovarian cancer 15799	Ovarian Cancer 17717AID	Ovarian Cancer 4004664B1	Ovarian Cancer	4005315A1	ovarian cancer 94127303	Ovarian Cancer 96069304	Ovarian Cancer 9707G029	Ovarian Cancer 9807G045	ovarian cancer 9809G001	Ovarian Cancer 9905C032RC	Ovarian cancer 9907 C00 3rd	Prostate	Prostate (clonetech)	prostate cancer	prostate cancer #15176	prostate cancer #15509	prostate cancer #15673	Small Intestine (Clontech)	0.1	Spleen	Thymus T cells activated
(9807G017)	Ovarian Cancer (9809G001)	ovarian cancer 15799	Ovarian Cancer 17717AID	Ovarian Cancer 4004664B1	Ovarian Cancer	4005315A1	ovarian cancer 94127303	Ovarian Cancer 96069304	Ovarian Cancer 9707G029	Ovarian Cancer 9807G045	ovarian cancer 9809G001	Ovarian Cancer 9905C032RC	Ovarian cancer 9907 C00	Prostate	Prostate (clonetech)	prostate cancer	prostate cancer #15176	prostate cancer #15509	prostate cancer #15673	Small Intestine	(Clontecn)	Spleen	Thymus T cells activated
	AR077	AR078	<b>├</b>	AR080	AR081		AR082	AR083	AR084	AR085	AR086	AR087	AR088	AR089	AR090	AR091	AR092	AR093	AR094		$\rightarrow$	$\rightarrow$	AR097

Tonsil geminal center centroblast Tonsil germinal center B T	Toucil		
	Tonsil geminal center		
	Centroblast  Toneil germinal center R		
	cell		
Tonsil lymph node	Tonsil lymph node		
Tonsil memory B cell	Tonsil memory B cell		
Whole Brain	Whole Brain		
Xenograft ES-2	Xenograft ES-2		
Xenograft SW626	Xenograft SW626		
001: IL-2	001: IL-2		
001: IL-2.1	001: IL-2.1		
001: IL-2 b	001: IL-2_b		
cytes	002 : Monocytes untreated	_	
	(1111)		
002: Monocytes   00	002 : Monocytes untreated (5hrs)		
002: Control.1C	002: Control.1C		
002: IL2.1C	002: IL2.1C		
003 : Placebo-treated Rat 0	003: Placebo-treated Rat		
Lacrimal Gland	Lacrimal Gland		
Rat	003: Placebo-treated Rat		
Submandibular Gland	Submandibular Gland		
004 : Monocytes 00	004: Monocytes untreated		
	(5hrs)		
rtes	004: Monocytes untreated		
untreated 1hr	lhr		
005: Placebo (48hrs)	005: Placebo (48hrs)		
006: pC4 (24hrs)	006: pC4 (24hrs)		
006: pC4 (48hrs)	006: pC4 (48hrs)		
007: PHA(1hr)	007: PHA(1hr)		

OO7: PHA/6HRS)	007: PMA(6hrs)	008: 1449 #2	01: A - max 24	01: A - max 26	01: A - max 30	01: B - max 24	01: B - max 26	01: B - max 30	1449 Sample	3T3P10 1.0uM insulin	3T3P10 10nM Insulin	3T3P10 10uM insulin	3T3P10 No Insulin	3T3P4	Adipose (41892)	Adipose Diabetic (41611)	Adipose Diabetic (41661)	Adipose Diabetic (41689)	Adipose Diabetic (41706)	Adipose Diabetic (42352)	Adipose Diabetic (42366)	Adipose Diabetic (42452)	Adipose Diabetic (42491)
007: PHA(6HRS)	007: PMA(6hrs)	008: 1449_#2	01: A - max 24	01: A - max 26	01: A - max 30	01: B - max 24	01: B - max 26	AR166 01: B - max 30	1449 Sample	3T3P10 1.0uM insulin	3T3P10 10nM Insulin	3T3P10 10uM insulin	3T3P10 No Insulin	3T3P4	Adipose (41892)	Adipose Diabetic (41611)	Adipose Diabetic (41661)	Adipose Diabetic (41689)	Adipose Diabetic (41706)	Adipose Diabetic (42352)	Adipose Diabetic (42366)	Adipose Diabetic (42452)	Adinose Diabetic
AR153	AR154	AR155	AR161	AR162	AR163	AR164	AR165	AR166	AR167	AR168	AR169	AR170	AR171	AR172	AR173	AR174	AR175	AR176	AR177	AR178	AR179	AR180	AR181

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(ODO4591B)	Colon Cancer (15663)	Colon Cancer (4005144A4)	Colon Cancer (4005413A4)	Colon Cancer (4005570B1)	Control RNA #1	Control RNA #2	Cultured Preadipocyte	Cultured Preadipocyte	Donor II B-Cells 24hrs	12	H114EP12 10nM Insulin	H114EP12 (10nM insulin)	H114EP12 (2.6ug/ul)	H114EP12 (3.6ug/ul)	HUVEC #1	HUVEC #2	L6 undiff.	L6 Undifferentiated	L6P8 + 10nM Insulin	T6P8 + HS	L6P8 10nM Insulin	Liver (00-06-A007B)	Liver (96-02-A075)	Liver (96-03-A144)	Liver (96-04-A138)
(ODQ4591B)	Colon Cancer (15663)	Colon Cancer (4005144A4)	Colon Cancer (4005413A4)	Colon Cancer (4005570B1)	Control RNA #1	Control RNA #2	Cultured Preadipocyte	Cultured Preadipocyte (Red)	Donor II B-Cells 24hrs	Donor II Resting B-Cells	H114EP12 10nM Insulin	H114EP12 (10nM insulin)	H114EP12 (2.6ug/ul)	H114EP12 (3.6ug/ul)	HUVEC #1	HUVEC #2	L6 undiff.	L6 Undifferentiated	L6P8 + 10nM Insulin	Teps + HS	L6P8 10nM Insulin	Liver (00-06-A007B)	Liver (96-02-A075)	Liver (96-03-A144)	Liver (96-04-A138)
	AR204	AR205	AR206	AR207	AR208	AR209	AR210	AR211	AR212	AR213	AR214	AR215	AR216	AR217	AR218	AR219	-	AR222	AR223	AR224	AR225	AR226	AR227		_

ver (97-10-A074B) ver (98-09-A242A) ver (98-09-A242A) ver Diabetic (1042) ver Diabetic (41616) ver Diabetic (42352R) ver Diabetic (42483) ver Diabetic (42491) ver Diabetic (99-09-A281A) Lung (27270) Lung (2727Q) Cancer (4005121A5)	Liver (98 Liver Dia Liver Dia Liver Diab Liver Diab Liver Dial Liv	Liver (97-10-A074B)         Liver (97-10-A074B)           Liver (98-09-A242A)         Liver (98-09-A242A)           Liver Diabetic (1042)         Liver Diabetic (1042)           Liver Diabetic (41616)         Liver Diabetic (41616)           Liver Diabetic (41955)         Liver Diabetic (42192)           Liver Diabetic (42350R)         Liver Diabetic (42192)           Liver Diabetic (42491)         Liver Diabetic (42191)           Liver Diabetic (42491)         Liver Diabetic (42191)           Liver Diabetic (42191)         Liver Diabetic (42191)           Lung (27270)         Lung (27270)           Lung (27270)         Lung (27270)           Lung (27270)         Lung (27270)           Lung (27270)         Lung (27270)           Lung Cancer (4005)         Lung Cancer (4005)
	Liv Liv Lung Lung Lung	c (42366) c (42483) c (42491) c (99-09-

AR257	Muscle (97-11-A056d)	Muscle (97-11-A056d)	
AR258	Muscle (99-06-A210A)	Muscle (99-06-A210A)	i
AR259	Muscle (99-07-A203B)	Muscle (99-07-A203B)	
AR260	Muscle (99-7-A203B)	Muscle (99-7-A203B)	
AR261	Muscle Diabetic	Muscle Diabetic (42352R)	
C7CQ V	Mr.golo Dichotic (42366)	March Birt die (1937)	
AK202	Muscle Diabetic (42366)	Muscle Diabetic (42366)	
AR263	NK-19 Control	NK-19 Control	
AR264	NK-19 IL Treated 72hrs	NK-19 IL Treated 72hrs	
AR265	NK-19 UK Treated 72	NK-19 UK Treated 72 hrs.	
	hrs.		
AR266		Omentum Normal (94-08-	
	08-B009)	B009)	
AR267	Normal (97-	Omentum Normal (97-01-	
	01-A039A)	A039A)	
AR268	Omentum Normal (97-	Omentum Normal (97-04-	
	04-A114C)	A114C)	
AR269	Omentum Normal (97-	Omentum Normal (97-06-	
	06-A117C)	A117C)	
AR270	Omentum Normal (97-	Omentum Normal (97-09-	
	09-B004C)	B004C)	
AR271	Ovarian Cancer	Ovarian Cancer	
	(17717AID)	(17717AID)	
AR272	Ovarian Cancer	Ovarian Cancer	
	(9905C023RC)	(9905C023RC)	
AR273	Ovarian Cancer	Ovarian Cancer	
	(9905C032RC)	(9905C032RC)	
AR274	Ovary (9508G045)	Ovary (9508G045)	
AR275	Ovary (9701G208)	Ovary (9701G208)	
AR276	Ovary 9806G005	Ovary 9806G005	
AR277	Pancreas	Pancreas	
AR278	Placebo	Placebo	
AR279	rIL2 Control	rIL2 Control	

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AK280	KSSZ88L	KSSZ88L	
AR281	RSS288LC	RSS288LC	
AR282	Salivary Gland	Salivary Gland	
AR283	Skeletal Muscle	Skeletal Muscle	
AR284	Skeletal Muscle (91-01-	Skeletal Muscle (91-01-	
AR285	Skeletal Muscle (42180)	Skeletal Muscle (42180)	
AR286		· I —	
AR287	Skeletal Muscle (42461)	Skeletal Muscle (42461)	
AR288	Skeletal Muscle (91-01-	Skeletal Muscle (91-01-	
	A105)	A105)	
AR289	Skeletal Muscle (92-04-	Skeletal Muscle (92-04-	
A R 200	Sheletal Muscle (96.08	Chalatal Muscale (06,00	
	A171)	A171)	
AR291	Skeletal Muscle (97-07-	Skeletal Muscle (97-07-	
	A190A)	A190A)	
AR292	Skeletal Muscle Diabetic	Skeletal Muscle Diabetic	
	(42352)	(42352)	
AR293	Skeletal Muscle Diabetic	Skeletal Muscle Diabetic	
	(42366)	(42366)	
AR294	Skeletal Muscle Diabetic (42395)	Skeletal Muscle Diabetic (42395)	
AR295	Skeletal Muscle Diabetic	Skeletal Muscle Diabetic	1
	(42483)	(42483)	
AR296	Skeletal Muscle Diabetic	Skeletal Muscle Diabetic	
	(42491)	(42491)	
AR297	Skeletal Muscle Diabetic	Skeletal Muscle Diabetic	
	42352	42352	
AR298	Skeletal Musle (42461)	Skeletal Musle (42461)	
AR299	Small Intestine	Small Intestine	
AR300	Stomach	Stomach	
AR301	T-Cell + HDPBQ71.fc	T-Cell + HDPBQ71.fc	

	1440 121	1440 161	
20701	T C-11 - 11700 21 C		
AK302	1-Cell + HDPBQ/1.fc 1449 6hrs	1-Cell + HDPBQ/1.tc 1449 6hrs	
AR303	T-Cell + IL2 16hrs	T-Cell + IL2 16hrs	
AR304	T-Cell + IL2 6hrs	T-Cell + IL2 6hrs	
AR306	T-Cell Untreated 16hrs	T-Cell Untreated 16hrs	
AR307	T-Cell Untreated 6hrs	T-Cell Untreated 6hrs	
AR308	T-Cells 24 hours	T-Cells 24 hours	
AR309	T-Cells 24 hrs	T-Cells 24 hrs	
AR310	T-Cells 24 hrs.	T-Cells 24 hrs.	
AR311	T-Cells 24hrs	T-Cells 24hrs	
AR312	T-Cells 4 days	T-Cells 4 days	
AR313	Thymus	Thymus	
AR314	TRE	TRE	
AR315	TREC	TREC	
AR317	B lymphocyte,	B lymphocyte,	
AR318		(non-T; non-B)	
AR326	001 - 293 RNA (Vector	001 - 293 RNA (Vector	
	Control)	Control)	
AR327	001: Control	001: Control	
AR328	001: Control.1	001: Control.1	
AR355	Acute Lymphocyte	Acute Lymphocyte	
		Leukemia	
AR356	AML Patient #11	AML Patient #11	
AR357	AML Patient #2	AML Patient #2	
AR358	AML Patient #2 SGAH	AML Patient #2 SGAH	
AR359	AML Patient#2	AML Patient#2	
AR360	Aorta	Aorta	
AR361	B Cell	B Cell	
AR362	B lymphoblast	B lymphoblast	
AR363	B lymphocyte	B lymphocyte	
AR364	B lymphocytes	B lymphocytes	

ABAKS	D 0.11	= 6		
COCHE	-	B-cell		
AR366		B-Cells		
AR367	-+	B-Lymphoblast		
AR368	-	B-Lymphocytes		
AR369	Bladder	Bladder		
AR370	_	Bone Marrow		
AR371	Bronchial Epithelial Cell	Bronchial Epithelial Cell		
AR372	Bronchial Epithelial	Bronchial Epithelial Cells		
	Cells			.,
AR373	Caco-2A	Caco-2A		
AR374	Caco-2B	Caco-2B		
AR375	Caco-2C	Caco-2C		
AR376	_	Cardiac #1		
AR377	Cardiac #2	Cardiac #2		
AR378	Chest Muscle	Chest Muscle	177.00	
AR381	Dendritic Cell	Dendritic Cell		
AR382	Dendritic cells	Dendritic cells		
AR383	E.coli	E.coli		
AR384	Epithelial Cells	Epithelial Cells		
AR385	Esophagus	Esophagus		
AR386	FPPS	FPPS		
AR387	FPPSC	FPPSC		
AR388	HepG2 Cell Line	HepG2 Cell Line		
AR389	HepG2 Cell line Buffer	HepG2 Cell line Buffer 1		
	l hr.			
AR390	HepG2 Cell line Buffer 06 hr	HepG2 Cell line Buffer 06 hr		
AR391	HepG2 Cell line Buffer 24 hr.	HepG2 Cell line Buffer 24 hr.		
AR392	HepG2 Cell line Insulin 01 hr.	HepG2 Cell line Insulin 01 hr.		
AR393	HepG2 Cell line Insulin	HepG2 Cell line Insulin 06		1

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HMCS HMCS HMSC HUVEC#3 HUVEC#4 KIDNEY NORMAL KIDNEY TUMOR KIDNEY TUMOR KIDNEY TUMOR Macrophage Macrophage Macrophage Monocyte Monocytes Monocytes Myocardium Myocardium Myocardium Myocardium	AL AL SR
HMCS HMSC HUVEC#3 HUVEC#4 KIDNEY NORMAL KIDNEY TUMOR KIDNEY TUMOR KIDNEY TUMOR  Macrophage Macrophage Megakarioblast Monocyte Monocytes Monocytes Myocardium Myocardium Myocardium Myocardium	AL OR It
HMSC HUVEC #3 HUVEC #4 KIDNEY TUMOR KIDNEY TUMOR KIDNEY TUMOR KIDNEY TUMOR  KIDNEY TUMOR  Macrophage Macrophage Megakarioblast Monocytes Monocytes Myocardium Myocardium Myocardium Myocardium	AL NR 18   19   19   19   19   19   19   19
HUVEC #3 HUVEC #4 KIDNEY NORMAL KIDNEY TUMOR KIDNEY TUMOR KIDNEY TUMOR  Macrophage Macrophage Macrophage Monocyte Monocytes Monocytes Myocardium Myocardium Myocardium#3	AL JR
HUVEC #4 KIDNEY NORMAL KIDNEY TUMOR KIDNEY TUMOR Lymph Node Macrophage Macrophage Monocyte Monocyte Monocytes Myocardium Myocardium Myocardium#3	AL JR IL
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KIDNEY TUMOR  Lymph Node  Macrophage  Megakarioblast  Monocyte  Monocytes  Myocardium  Myocardium  Myocardium #3	
Lymph Node  Macrophage  Megakarioblast  Monocyte  Monocytes  Myocardium  Myocardium  Myocardium	
Lymph Node Macrophage Megakarioblast Monocyte Monocytes Myocardium Myocardium#3	
Lymph Node  Macrophage  Megakarioblast  Monocyte  Monocytes  Myocardium  Myocardium #3	
Macrophage Megakarioblast Monocyte Monocytes Myocardium Myocardium #3	
Megakarioblast Monocyte Monocytes Myocardium Myocardium #3	
Monocyte Monocytes Myocardium Myocardium #3	
Monocytes Myocardium #3	
Myocardium #3	
Myocardium #3	
	8
Myocardium #4	
AR415 Myocardium #5 Myocardium #5	
AR416 NK NK	
AR417 NK cell	
AR418 NK cells NK cells	
AR419 NKYa NKYa	
AR420 NKYa019 NKYa019	
AR421 Ovary	
AR422 Patient #11 Patient #11	
AR423 Peripheral blood Peripheral blood	P
AR424 Primary Adipocytes Primary Adipocytes	tes
AR425 Promyeloblast Promyeloblast	

$\vdash$	RSSWT	RSSWT		
$\dashv$	RSSWTC	RSSWTC		
_	SW 480(G1)	SW 480(G1)		
$\overline{}$	SW 480(G2)	SW 480(G2)		
_	W 480(G3)	SW 480(G3)		
-	SW 480(G4)	SW 480(G4)		
	SW 480(G5)	SW 480(G5)		
AR434 T	T Lymphoblast	T Lymphoblast		
AR435 T	T Lymphocyte	T Lymphocyte		
	T-Cell	T-Cell		
AR438 T	T-Cell,	T-Cell,		
AR439 T	T-Cells	T-Cells		
	T-lymphoblast	T-lymphoblast		
AR441 T	Th 1	Th 1		
AR442 T	Th 2	Th 2		
AR443 T	Th1	Th1		
	Th2	Th2		
-	Human Adult Heart	Human Adult Heart	Heart	Uni-ZAP XR
┪	Human Adult Spleen	Human Adult Spleen	Spleen	Uni-ZAP XR
$\neg \uparrow$	Human Cerebellum	Human Cerebellum	Brain	Uni-ZAP XR
H0008   W	Whole 6 Week Old Embryo			Uni-ZAP XR
Н 6000Н	Human Fetal Brain			Uni-ZAP XR
+	Human Fetal Kidney	Human Fetal Kidney	Kidney	Uni-ZAP XR
-	Human Fetal Kidney	Human Fetal Kidney	Kidney	Uni-ZAP XR
H0013   H	Human 8 Week Whole Embryo	Human 8 Week Old Embryo	Embryo	Uni-ZAP XR
$\rightarrow$	Human Gall Bladder	Human Gall Bladder	Gall Bladder	Uni-ZAP XR
H0015   H	Human Gall Bladder, fraction II	Human Gall Bladder	Gall Bladder	Uni-ZAP XR
H0016 H	Human Greater Omentum	Human Greater Omentum	peritoneum	Uni-ZAP XR
1				

H0017	Human Greater	Human Greater Omentum	peritoneum		Uni-ZAP XR
7	Omentum		•		
H0020	Human Hippocampus	Human Hippocampus	Brain		Uni-ZAP XR
H0022	Jurkat Cells	Jurkat T-Cell Line			Lambda ZAP II
H0023	Human Fetal Lung				Uni-ZAP XR
H0024	Human Fetal Lung III	Human Fetal Lung	Lung		Uni-ZAP XR
H0025	Human Adult Lymph Node	Human Adult Lymph Node	Lymph Node		Lambda ZAP II
H0026	Namalwa Cells	Namalwa B-Cell Line, EBV immortalized			Lambda ZAP II
H0030	Human Placenta				Uni-ZAP XR
H0031	Human Placenta	Human Placenta	Placenta		Uni-ZAP XR
H0032	Human Prostate	Human Prostate	Prostate		Uni-ZAP XR
H0033	Human Pituitary	Human Pituitary			Uni-ZAP XR
H0036	Human Adult Small Intestine	Human Adult Small Intestine	Small Int.		Uni-ZAP XR
H0038	Human Testes	Human Testes	Testis		Uni-ZAP XR
H0039	Human Pancreas Tumor	Human Pancreas Tumor	Pancreas	disease	Uni-ZAP XR
H0040	Human Testes Tumor	Human Testes Tumor	Testis	disease	Uni-ZAP XR
H0041	Human Fetal Bone	Human Fetal Bone	Bone		Uni-ZAP XR
H0042	Human Adult Pulmonary	Human Adult Pulmonary	Lung		Uni-ZAP XR
H0044	Human Cornea	Human Cornea	eye		Uni-ZAP XR
H0045	Human Esophagus, Cancer	Human Esophagus, cancer	Esophagus	disease	Uni-ZAP XR
H0046	Human Endometrial	Human Endometrial	Uterus	disease	Uni-ZAP XR
	Tumor	Tumor			
H0047	Human Fetal Liver	Human Fetal Liver	Liver		Uni-ZAP XR
H0048	Human Pineal Gland	Human Pineal Gland			Uni-ZAP XR
H0050	Human Fetal Heart	Human Fetal Heart	Heart		Uni-ZAP XR
H0051	Human Hippocampus	Human Hippocampus	Brain		Uni-ZAP XR
H0052	Human Cerebellum	Human Cerebellum	Brain		Uni-ZAP XR
H0056	Human Umbilical Vein,	Human Umbilical Vein	Umbilical vein		Uni-ZAP XR

	Uni-ZAP XR	Lambda ZAP II	Lambda ZAP II	pBluescript	pBluescript	Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR		Lambda ZAP II	Uni-ZAP XR	Uni-ZAP XR		Lambda ZAP II	Uni-ZAP XR		pBluescript	Uni-ZAP XR		pBluescript
		disease	disease						disease										disease					disease			disease		
				Cell Line	Cell Line					Cell Line					Cell Line		Cell Line		,										
		Thymus	Uterus	Blood	Blood	Thymus	Esophagus		Skin	Blood		Pancreas	Adrenal gland		Blood		Blood		Lung	Skin	· mpddday'r yernau			Sk Muscle			T-Cell		Heart
Endothelial Cells		Human Thymus Tumor	Human Uterine Cancer	Human Macrophage	Human Macrophage	Human Thymus	Human Esophagus, normal		Human Skin Tumor	Activated T-Cells		Human Pancreas	Human Infant Adrenal	Cland	Activated T-Cells		Human Membrane Bound	Polysomes	Human Lung Cancer	Human Fetal Skin	Jurkat Cells		Human Colon	Epithelioid Sarcoma,	muscle	Human Thymus	T-Cell Lymphoma		Human Adult Heart
Endo. remake	Human Fetal Spleen	Human Thymus Tumor	Human Uterine Cancer	Human Macrophage	Human Macrophage	Human Thymus	Human Esophagus,	Normal	Human Skin Tumor	Human Activated T-	Cells	Human Pancreas	Human Infant Adrenal	Gland	Human Activated T-	Cells (II)	Human Membrane	Bound Polysomes	Human Lung Cancer	Human Fetal Epithelium (Skin)	HUMAN JURKAT	MEMBRANE BOUND POLYSOMES	Human Colon	Human epithelioid	sarcoma	Human Thymus	Human T-Cell	Lymphoma	Human Adult Heart, subtracted
	H0057		-	H0060		-+	H0065		8900H	6900H	$\dashv$	H0070	H0071	+	H0075		9L00H		H0078	H0081	H0083		H0085	9800H		H0087	0600H	-+	H0097

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Uni-ZAP XR	pBluescript	Uni-ZAP XR	pBluescript	Uni-ZAP XR	pBluescript	Uni-ZAP XR	pBluescript	pBluescript	pBluescript	pBluescript	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR
																disease	
							Cell Line										Cell Line
Liver	Lung	Embryo	Embryo	Brain	Adrenal gland	Lymph Node	Blood	Ovary	Placenta	Thymus	Kidney	Spleen	eye	Sk Muscle	Brain	Sk Muscle	Blood
Human Adult Liver	Human Lung Cancer	Human Whole Six Week Old Embryo	Human Whole Six Week Old Embryo	Human Fetal Brain	Human Infant Adrenal Gland	Human Adult Lymph Node	Macrophage	Human Old Ovary	Human Placenta	Human Thymus Tumor	Human Adult Kidney	Human Adult Spleen	Human Cornea	Human Skeletal Muscle	Human Fetal Dura Mater	Human Rhabdomyosarcoma	Cyclohexamide Treated
Human Adult Liver, subtracted	Human Lung Cancer, subtracted	Human Whole Six Week Old Embryo	Human Whole 6 Week Old Embryo (II), subt	Human Fetal Brain, subtracted	Human Infant Adrenal Gland, subtracted	Human Adult Lymph Node, subtracted	Human Macrophage, subtracted	Human Old Ovary, subtracted	Human Placenta, subtracted	Human Thymus Tumor, subtracted	Human Adult Kidney	Human Adult Spleen, subtracted	Human Cornea, subtracted	Human Adult Skeletal Muscle	Human Fetal Dura Mater	Human Rhabdomyosarcoma	Cem cells cyclohexamide
	H0099	H0100	H0102	H0103	H0107	H0108	H0109	H0110	H0111	H0116	H0118	H0120	H0121	H0122	-	H0124	H0125

	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR	Ilm: 7AP VR	11.: 7AD VD	UIII-ZAF AR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR
							! !						i			   			disease	disease		
		Cell Line	Cell Line	Cell Line	Cell Line		Cell Line		Cell Line	Cell Line	Cell Line										Cell Line	Cell Line
		Prostate	Prostate	Prostate	Blood	Synovium	Blood		Blood	Blood	Blood		Embryo	Liver	Dahan	Emoryo	Testis	Liver	Skin	Adrenal Gland	Blood	Blood
Cem, Jurkat, Raji, and Supt	Jurkat Cells	LNCAP Cell Line	LNCAP Cell Line	LNCAP Cell Line	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Human Synovial Sarcoma	Cyclohexamide Treated	Cem, Jurkat, Kaji, and Supt	Activated T-Cells	Activated T-Cells	Activated T-Cells		9 Wk Old Early Stage	Human Adult I war	Human Whole 7 Wool	ruman whole / week Old Embryo	Epididymis	Human Fetal Liver	Human Skin Fibrosarcoma	Human Adrenal Gland Tumor	Activated T-Cells	Activated T-Cells
treated	Jurkat cells, thiouridine activated	LNCAP untreated	LNCAP + 0.3nM R1881	LNCAP + 30nM R1881	Raji Cells, cyclohexamide treated	Human Synovial Sarcoma	Supt Cells,	cyclonexamide treated	Activated T-Cells, 4 hrs.	Activated T-Cells, 8 hrs.	Activated T-Cells, 12	hrs.	Nine Week Old Early	Stage Fittillall	7 Woolf Old Early, Chan	week Old Early Stage Human, subtracted	Human Epididymus	Early Stage Human Liver	Human Fibrosarcoma	Human Adrenal Gland Tumor	Activated T-Cells, 4 hrs., ligation 2	Activated T-Cells, 8 hrs.,
	H0128	H0130	H0131	H0132	H0134	H0135	H0136		H0139	H0140	H0141		H0144	H01/7	十		H0150	H0151	H0154	H0156	H0158	H0159

H0161	Activated T-Cells, 24	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
	hrs., ligation 2					
H0163	Human Synovium	Human Synovium	Synovium			Uni-ZAP XR
H0165	Human Prostate Cancer, Stage B2	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0166	Human Prostate Cancer, Stage B2 fraction	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0167	Activated T-Cells, 24 hrs.	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0169	Human Prostate Cancer, Stage C fraction	Human Prostate Cancer, stage C	Prostate		disease	Uni-ZAP XR
H0170	12 Week Old Early Stage Human	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0171	12 Week Old Early Stage Human, II	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0172	Human Fetal Brain, random primed	Human Fetal Brain	Brain			Lambda ZAP II
H0176	CAMA1Ee Cell Line	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0177	CAMA I Ee Cell Line	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0178	Human Fetal Brain	Human Fetal Brain	Brain			Uni-ZAP XR
H0179	Human Neutrophil	Human Neutrophil	Blood	Cell Line		Uni-ZAP XR
H0180	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0181	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0182	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0183	Human Colon Cancer	Human Colon Cancer	Colon		disease	Uni-ZAP XR
H0184	Human Colon Cancer, metasticized to live	Human Colon Cancer, metasticized to liver	Liver		disease	Lambda ZAP II
H0187	Resting T-Cell	T-Cells	Blood	Cell Line		Lambda ZAP II
H0188	Human Normal Breast	Human Normal Breast	Breast			Uni-ZAP XR
H0189	Human Resting	Human	Blood	Cell Line		Uni-ZAP XR

	Macrophage	Macrophage/Monocytes			
	Human Activated	Human	Blood	Cell Line	Uni-ZAP XR
	Macrophage (LPS)	Macrophage/Monocytes			
	Cem Cells, cyclohexamide treated, subtra	Cyclohexamide Treated Cem, Jurkat, Raji, and Sunt	Blood	Cell Line	Uni-ZAP XR
	Human Cerebellum, subtracted	Human Cerebellum	Brain		pBluescript
	Human Cardiomyopathy, subtracted	Human Cardiomyopathy	Heart		Uni-ZAP XR
	Human Fetal Liver, subtracted	Human Fetal Liver	Liver		Uni-ZAP XR
	Human Fetal Liver, subtracted, neg clone	Human Fetal Liver	Liver		Uni-ZAP XR
	Human Greater Omentum, fract II remake,	Human Greater Omentum	peritoneum		Uni-ZAP XR
_	Human Hippocampus, subtracted	Human Hippocampus	Brain		pBluescript
	Jurkat Cells, cyclohexamide treated, subtraction	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line	Uni-ZAP XR
	Human Colon Cancer, subtracted	Human Colon Cancer	Colon		pBluescript
	Human Colon Cancer, differential	Human Colon Cancer	Colon		pBluescript
	LNCAP, differential expression	LNCAP Cell Line	Prostate	Cell Line	pBluescript
	Early Stage Human Lung, subtracted	Human Fetal Lung	Lung		pBluescript
	Human Cerebellum, differentially expressed	Human Cerebellum	Brain		Uni-ZAP XR
	Human	Human Prostate	Prostate		pBluescript

	Prostate, differential				
H0212	Human Prostate, subtracted	Human Prostate	Prostate		pBluescript
H0213	Human Pituitary, subtracted	Human Pituitary			Uni-ZAP XR
H0214	Raji cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line	pBluescript
H0215	Raji cells, cyclohexamide treated, differentially expressed	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line	pBluescript
H0216	Supt cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line	pBluescript
H0217	Supt cells, cyclohexamide treated, differentially expressed	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line	pBluescript
H0218	Activated T-Cells, 0hrs, subtracted	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0219	Activated T-Cells, 0hrs, differentially expressed	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0220	Activated T-Cells, 4 hrs, subtracted	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0222	Activated T-Cells, 8 hrs, subtracted	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0223	Activated T-Cells, 8 hrs, differentially expressed	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0224	Activated T-Cells, 12 hrs, subtracted	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0225	Activated T-Cells, 12hrs, differentially expressed	Activated T-Cells	Blood	Cell Line	Uni-ZAP XR
H0229	Early Stage Human	Early Stage Human Brain	Brain		Lambda ZAP II

$\vdash$	Brain, random primed					
	Human Cardiomyopathy, diff exp	Human Cardiomyopathy	Heart		disease	Uni-ZAP XR
ı -	Human Colon, subtraction	Human Colon				pBluescript
	Human Colon, differential expression	Human Colon				pBluescript
ļ	human colon cancer, metastatic to liver, differentially expressed	Human Colon Cancer, metasticized to liver	Liver			pBluescript
<del> </del>	Human colon cancer, metaticized to liver, subtraction	Human Colon Cancer, metasticized to liver	Liver			pBluescript
+	Human Kidney Tumor	Human Kidney Tumor	Kidney		disease	Uni-ZAP XR
<del></del>	C7MCF7 cell line, estrogen treated, Differential	C7MCF7 Cell Line, estrogen freated	Breast	Cell Line		Uni-ZAP XR
ļ	C7MCF7 cell line, estrogen treated, subtraction	C7MCF7 Cell Line, estrogen treated	Breast	Cell Line		Uni-ZAP XR
H0242	Human Fetal Heart, Differential (Fetal- Specific)	Human Fetal Heart	Heart			pBluescript
<del>                                     </del>	Human 8 Week Whole Embryo, subtracted	Human 8 Week Old Embryo	Embryo			Uni-ZAP XR
H0246	Human Fetal Liver- Enzyme subtraction	Human Fetal Liver	Liver			Uni-ZAP XR
H0247	Human Membrane Bound Polysomes- Enzyme Subtraction	Human Membrane Bound Polysomes	Blood	Cell Line		Uni-ZAP XR
<del>    -   -   -   -   -   -   -</del>	HE7, subtracted by hybridization with E7 cDNA	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR

Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Lambda ZAP II	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Lambda ZAP II	Uni-ZAP XR	Uni-ZAP XR	Lambda ZAP II	Lambda ZAP II	Lambda ZAP II	Lambda ZAP II
	disease	disease							disease						
						Cell Line	Cell Line				Cell Line	Cell Line	Cell Line	Cell Line	Cell Line
	Cartilage	Bone	Testis	Lymph Node	Lymph Node	Blood	Blood	Brain	Colon	Tonsil	Blood	Vein	Vein	Umbilical vein	Umbilical vein
Human Monocytes	Human Chondrosarcoma	Human Osteosarcoma	Human Adult Testis	Breast Lymph Node	Breast Lymph Node	Human HL-60 Cells, unstimulated	HL-60 Cells, PMA stimulated 4H	Human Cerebellum	Human Colon Cancer	Human Tonsil	T-Cells	НМЕС	HMEC	HUVE Cells	HUVE Cells
Human Activated Monocytes	Human Chondrosarcoma	Human Osteosarcoma	Human adult testis, large inserts	Breast Lymph node cDNA library	breast lymph node CDNA library	H0256 HL-60, unstimulated	HL-60, PMA 4H	H. cerebellum, Enzyme subtracted	human colon cancer	human tonsils	Activated T-Cell (12hs)/Thiouridine labelledEco	Human Microvascular Endothelial Cells, fract. A	Human Microvascular Endothelial Cells, fract. B	Human Umbilical Vein Endothelial Cells, fract. A	Human Umbilical Vein Endothelial Cells, fract. B
H0250	H0251	H0252	H0253	H0254	H0255	H0256	H0257	H0261	H0263	H0264	H0265	Н0266	H0267	H0268	H0269

Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	pBluescript	ZAP Express	ZAP Express	Uni-ZAP XR	Uni-ZAP XR		Uni-ZAP XR		Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	ZAP Express
	Cell Line				Cell Line	Cell Line		Cell Line		Cell Line		Cell Line	Cell Line	Cell Line		Cell Line	Cell Line	
Pancreas	Blood	Tonsil	Spleen	Adrenal gland	cell line	Lymph Node	Breast	Bone		Bone		Bone	Bone	Bone		Placenta	Placenta	Cord Blood
Human Pancreas	Human Neutrophil - Activated	Human Tonsil	Human Adult Spleen	Human Infant Adrenal Gland	K562 Cell line	Lymph Node, abnormal cell line	Human Primary Breast Cancer	Human Osteoblastoma	MG63 cell line	Human Osteoblastoma	MG63 cell line	Human Osteoblastoma HOS cell line	Human Osteoblastoma HOS cell line	Human Osteoblastoma HOS cell line		Amniotic Cells - TNF induced	Amniotic Cells - Primary	CD34 Positive Cells
HPAS (human pancreas, subtracted)	Human Neutrophil, Activated	HUMAN TONSILS, FRACTION 2	Human Adult Spleen, fractionII	Human Infant Adrenal Gland, Subtracted	K562 + PMA (36 hrs)	Lymph node, abnorm. cell line (ATCC #7225)	HBGB"s differential	Human OB MG63	control fraction I	Human OB MG63	treated (10 nM E2) fraction I	Human OB HOS control fraction I	Human OB HOS treated (1 nM E2) fraction I	Human OB HOS treated (10 nM E2) fraction I	WI 38 cells	Amniotic Cells - TNF	Amniotic Cells - Primary	CD34 positive cells (Cord Blood)
H0270	H0271	H0272	H0274	H0275	H0280	H0281	H0282	H0284		H0286		H0288	H0290	H0292	H0293	H0294	H0295	H0300

CD34 positive cells (Cord Blood)	CD34 Positive Cells	Cord Blood			ZAP Express
	CD34 Depleted Buffy Coat (Cord Blood)	Cord Blood			ZAP Express
	Synovium, Chronic Synovitis/ Osteoarthritis	Synovium		disease	Uni-ZAP XR
I	Brain	Brain			Uni-ZAP XR
l	Human Stomach	Stomach			Uni-ZAP XR
ı —	Human B Cell Lymphoma	Lymph Node		disease	Uni-ZAP XR
1	Human Frontal Cortex	Brain			Uni-ZAP XR
I	Schwanoma	Nerve		disease	Uni-ZAP XR
l '	Human Corpus Callosum	Brain			Uni-ZAP XR
1	Ovarian Cancer	Ovary		disease	Uni-ZAP XR
ı	Dermatofibrosarcoma	Skin		disease	Uni-ZAP XR
- 1	Protuberans				
	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
	Hemangiopericytoma	Blood vessel		disease	Lambda ZAP II
	Kidney Cancer	Kidney		disease	Uni-ZAP XR
1	Duodenum				Uni-ZAP XR
I	Bone Marrow Cell Line RS4;11	Bone Marrow	Cell Line		Uni-ZAP XR
1	Lingual Gyrus	Brain			Uni-Zap XR
l	Stomach Cancer - 5383A (human)			disease	Uni-ZAP XR
L	Adipose - 6825A (human)				Uni-ZAP XR
L	Skin - 4000868H	Skin			Uni-ZAP XR
1	Brain (Medulloblastoma)- 9405C006R	Brain		disease	Uni-ZAP XR
ļ	Human Adult Liver	Liver			pCMVSport 1
	Human Fetal Liver, mixed	Liver			Uni-ZAP XR

	mixed 10 & 14 week	10&14 Week				
H0351	Glioblastoma	Glioblastoma	Brain		disease	Uni-ZAP XR
H0352	wilm"s tumor	Wilm"s Tumor			disease	Uni-ZAP XR
H0354	Human Leukocytes	Human Leukocytes	Blood	Cell Line		pCMVSport 1
H0355	Human Liver	Human Liver, normal Adult				pCMVSport 1
H0356	Human Kidney	Human Kidney	Kidney			pCMVSport 1
H0357	H. Normalized Fetal Liver, II	Human Fetal Liver	Liver			Uni-ZAP XR
H0359	KMH2 cell line	KMH2				ZAP Express
H0360	Hemangiopericytoma	Hemangiopericytoma			disease	
H0361	Human rejected kidney	Human Rejected Kidney			disease	pBluescript
H0362	HeLa cell line	HELA CELL LINE				pSport1
H0366	L428 cell line	L428				ZAP Express
H0369	H. Atrophic Endometrium	Atrophic Endometrium and myometrium				Uni-ZAP XR
H0370	H. Lymph node breast	Lymph node with Met.			disease	Uni-ZAP XR
	Cancer	Breast Cancer				
H0372	Human Testes	Human Testes	Testis			pCMVSport 1
H0373	Human Heart	Human Adult Heart	Heart			pCMVSport 1
H0374	Human Brain	Human Brain				pCMVSport 1
H0375	Human Lung	Human Lung				pCMVSport 1
H0376	Human Spleen	Human Adult Spleen	Spleen			pCMVSport 1
H0379	Human Tongue, frac 1	Human Tongue				pSport1
H0380	Human Tongue, frac 2	Human Tongue				pSport1
H0381	Bone Cancer	Bone Cancer			disease	Uni-ZAP XR
H0383	Human Prostate BPH, re- excision	Human Prostate BPH				Uni-ZAP XR
H0384	Brain, Kozak	Human Brain				pCMVSport 1
H0386	Leukocyte and Lung; 4 screens	Human Leukocytes	Blood	Cell Line		pCMVSport 1
H0388	Human Rejected Kidney,	Human Rejected Kidney			disease	pBluescript

	pBluescript	pSport1	pSport1	pBluescript	ZAP Express	ZAP Express	ZAP Express	Lambda ZAP II	I ambda 7AP II	Lainoua Col II	ZAP Express		Uni-ZAP XR			Uni-ZAP XR		pBluescript		Uni-ZAP XR	pBluescript	pBluescript		pSport1	pSport1
	disease																								
													Cell Line			Cell Line									
		brain	brain	Liver						Brain	Cord Blood	-	I Imbilical vein			Umbilical vein						Brain		Bladder	Bladder
	Human Amygdala Depression	Human Meningima	Human Meningima	Human Fetal Liver	Redd-Sternberg cell	Redd-Sternberg cell	Redd-Sternberg cell	Human Kidney Cortex		Human Brain, Striatum Depression	CD34 Depleted Buffy	Coat (Cord Blood)	HI IVE Cells	110 4 E Cents		HUVE Cells		Human Pituitary		Human Amygdala Depression	Human Kidney Cortex	Human Brain, Striatum	Depression	H Male Bladder, Adult	Human Female Adult Bladder
704 re-excision	Human Amygdala Depression, re-excision	H. Meniingima, M6	H. Meningima, M1	Fetal Liver, subtraction II	A-14 cell line	A1-CELL LINE	L1 Cell line	Human Kidney Cortex,	re-rescue	Human Striatum Depression, re-rescue	CD34 depleted Buffy	Coat (Cord Blood), re-	U Habilion Voin	n. Ullullical Velli	Endothelial Cells, IL4	H. Umbilical Vein	endothelial cells,	Human Pituitary,	subtracted VI	H Amygdala Depression, subtracted	Human kidney Cortex,	H. Striatum Depression,	subtracted	H. Male bladder, adult	H Female Bladder, Adult
	H0390	H0391	+	1	H0394	H0395	H0396			H0400	H0402		110402			H0404		H0405		H0406	H0408	H0409		H0410	H0411

pSport1	pSport1	pSport1	pCMVSport 2.0	pBluescript	pBluescript	pBluescript	Uni-ZAP XR	pBluescript		pSport1	pSport1	pBluescript	pSport1	pSport1	ZAP Express	pBluescript	pBluescript		pBluescript
d	d	disease p	disease p	d	d	d	1	d		0.	g   p	l p	ď	d	Z	d.	<u>D</u>		d
Cell Line	Cell Line			Cell Line						Cell Line	Cell Line				Cell Line		Cell Line		
Umbilical vein	Umbilical vein	Ovary	Ovary	Blood						Blood	Blood			Ovary	cell line	Kidney	Umbilical vein		
HUVE Cells	HUVE Cells	Ovarian Tumor, OV5232	Ovarian Tumor, OV5232	Human Neutrophil - Activated	Human Pituitary	Human Pituitary	Bone Cancer	Bone Marrow		T-Cells	T-Cells	Human Pituitary	Human Adipose, left hiplipoma	Human Ovary Tumor	K562 Cell line	Kidney medulla	HUVE Cells		Human Brain, Striatum
Human umbilical vein endothelial cells, IL-4 induced	Human Umbilical Vein Endothelial Cells, uninduced	Ovarian Tumor I, OV5232	H. Ovarian Tumor, II, OV5232	Human Neutrophils, Activated, re-excision	Human Pituitary, subtracted VIII	Human Pituitary, subtracted VII	Bone Cancer, re-excision	Human Bone Marrow,	re-excision	T-Cell PHA 16 hrs	T-Cell PHA 24 hrs	Human Pituitary, subt IX	Human Adipose	Human Ovary	K562 + PMA (36 hrs),re- excision	H. Kidney Medulla, re- excision	Human Umbilical Vein	Endothelial cells, frac B, re-excision	Human Brain, striatum,
H0412	H0413	H0414	H0415	H0416	H0417	H0418	H0419	H0421		H0422	H0423	H0424	H0427	H0428	H0429	H0431	H0433		H0434

	re-excision					
H0435	Ovarian Tumor 10-3-95	Ovarian Tumor, OV350721	Ovary		1	pCMVSport 2.0
H0436	Resting T-Cell Library,II	T-Cells	Blood	Cell Line		pSport1
H0437	H Umbilical Vein	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
	Endothelial Cells, frac A,					
	re-excision					
H0438	H. Whole Brain #2, re-	Human Whole Brain #2				ZAP Express
	excision					•
H0439	Human Eosinophils	Eosinophils				pBluescript
H0441	H. Kidney Cortex,	Kidney cortex	Kidney			pBluescript
	subtracted		•			
H0443	H. Adipose, subtracted	Human Adipose, left				pSport1
		hiplipoma				·
H0444	Spleen metastic	Spleen, Metastic	Spleen		disease	pSport1
	melanoma	malignant melanoma	•			
H0445	Spleen, Chronic	Human Spleen, CLL	Spleen		disease	pSport1
	lymphocytic leukemia		•			
H0449	CD34+ cell, I	CD34 positive cells				pSport1
H0455	H. Striatum Depression,	Human Brain, Striatum	Brain			pBluescript
	subt	Depression		:		•
H0457	Human Eosinophils	Human Eosinophils				pSport1
H0458	CD34+ cell, I, frac II	CD34 positive cells				pSport1
H0459	CD34+cells, II,	CD34 positive cells				pCMVSport 2.0
	FRACTION 2					
H0461	H. Kidney Medulla,	Kidney medulla	Kidney			pBluescript
	subtracted					•
H0462	H. Amygdala		Brain			pBluescript
	Depression, subtracted			•		<b>1</b>
H0477	Human Tonsil, Lib 3	Human Tonsil	Tonsil			pSport1
H0478	Salivary Gland, Lib 2	Human Salivary Gland	Salivary gland			pSport1
H0479	Salivary Gland, Lib 3	Human Salivary Gland	Salivary gland			pSport1
H0483	Breast Cancer cell line,	Breast Cancer Cell line,				pSport1

	MDA 36	MDA 36				
H0484	Breast Cancer Cell line,	Breast Cancer Cell line,				pSport1
	angiogenic	Angiogenic, 36T3				
H0485	Hodgkin"s Lymphoma I	Hodgkin"s Lymphoma I			disease	pCMVSport 2.0
H0486	Hodgkin"s Lymphoma II	Hodgkin's Lymphoma II			disease	pCMVSport 2.0
H0487	Human Tonsils, lib I	Human Tonsils				pCMVSport 2.0
H0488	Human Tonsils, Lib 2	Human Tonsils				pCMVSport 2.0
H0489	Crohn"s Disease	Ileum	Intestine		disease	pSport1
H0490	Hl-60, untreated,	Human HL-60 Cells,	Blood	Cell Line		Uni-ZAP XR
	subtracted	unstimulated				
H0491	HL-60, PMA 4H,	HL-60 Cells, PMA	Blood	Cell Line		Uni-ZAP XR
	subtracted	stimulated 4H		,		
H0492	HL-60, RA 4h,	HL-60 Cells, RA	Blood	Cell Line		Uni-ZAP XR
	Subtracted	stimulated for 4H				
H0494	Keratinocyte	Keratinocyte				pCMVSport 2.0
H0497	HEL cell line	HEL cell line		HEL 92.1.7		pSport1
H0505	Human Astrocyte	Human Astrocyte				pSport1
H0506	Ulcerative Colitis	Colon	Colon			pSport1
H0509	Liver, Hepatoma	Human Liver, Hepatoma,	Liver		disease	pCMVSport 3.0
		patient 8				
H0510	Human Liver, normal	Human Liver, normal, Patient # 8	Liver			pCMVSport 3.0
H0512	Keratinocyte, lib 3	Keratinocyte				pCMVSport 2.0
H0518	pBMC stimulated w/ poly I/C	pBMC stimulated with poly I/C				pCMVSport 3.0
H0519	NTERA2, control	NTERA2, Teratocarcinoma cell line				pCMVSport 3.0
H0520	NTERA2 + retinoic acid,	NTERA2, Teratocarcinoma cell line				pSport1
H0521	Primary Dendritic Cells,	Primary Dendritic cells				pCMVSport 3.0
H0522	Primary Dendritic	Primary Dendritic cells				nCMVSnort 3.0
	cells,frac 2					

K,   Ig.	PCR, pBMC I/C treated Poly[I]/Poly[C] Normal Lung Fibroblasts	pBMC stimulated with poly I/C Poly[I]/Poly[C] Normal Lung Fibroblasts			PCRII pCMVSport 3.0
Myoloid Line Human ]	Myoloid Progenitor Cell Line Human Dermal	TF-1 Cell Line; Myoloid progenitor cell line Human Dermal			pCMVSport 3.0 pSport1
Endothelial Cells, untre	Endothelial Cells,untreated	Endothelial Cells, untreated			
erke	Merkel Cells	Merkel cells	Lymph node	dicoop	pSport1
rancrea Tumor	rancreas Islet Cell Tumor	rancreas Islet Cell Tumour	rancreas	disease	рэроги
Ë,	Skin, burned	Skin, leg burned	Skin		pSport1
딍	T Cell helper I	Helper T cell			pCMVSport 3.0
등 등	T cell helper II	Helper T cell			pCMVSport 3.0
uma	Human endometrial stromal cells	Human endometrial stromal cells			pCMVSport 3.0
ıma	Human endometrial	Human endometrial			pCMVSport 3.0
omo	stromal cells-treated with progesterone	stromal cells-treated with proge			
₽Ë	Human endometrial	Human endometrial			pCMVSport 3.0
rac	stromal cells-treated with estradiol	stromal cells-treated with estra			
凹	NTERA2	NTERA2,			pSport1
et ato	teratocarcinoma cell line+retinoic acid (14	Teratocarcinoma cell line			
days)	,				
H. Epic corpus	H. Epididiymus, caput & corpus	Human Epididiymus, caput and corpus			Uni-ZAP XR
д	H. Epididiymus, cauda	Human Epididiymus, cauda			Uni-ZAP XR
Huma Cells	Human Thymus Stromal Cells	Human Thymus Stromal Cells			pCMVSport 3.0
ĺ					

H0553	Human Placenta	Human Placenta				pCMVSport 3.0
H0555	Rejected Kidney, lib 4	Human Rejected Kidney	Kidney		disease	pCMVSport 3.0
H0556	Activated T-cell(12h)/Thiouridine-re-	T-Cells	Blood	Cell Line		Uni-ZAP XR
H0559	HL-60, PMA 4H, re-	HL-60 Cells, PMA	Blood	Cell Line		Uni-ZAP XR
0950H	KMH2	KMH2				nCMVSnort 3.0
H0561	L428	L428				pCMVSport 3.0
H0562	Human Fetal Brain, normalized c5-11-26	Human Fetal Brain				pCMVSport 2.0
H0563	Human Fetal Brain, normalized 50021F	Human Fetal Brain				pCMVSport 2.0
H0564	Human Fetal Brain, normalized C5001F	Human Fetal Brain				pCMVSport 2.0
9950Н	Human Fetal Brain,normalized c50F	Human Fetal Brain				pCMVSport 2.0
Н0567	Human Fetal Brain, normalized A5002F	Human Fetal Brain				pCMVSport 2.0
6950Н	Human Fetal Brain, normalized CO	Human Fetal Brain				pCMVSport 2.0
H0570	Human Fetal Brain, normalized C500H	Human Fetal Brain				pCMVSport 2.0
H0571	Human Fetal Brain, normalized C500HE	Human Fetal Brain				pCMVSport 2.0
H0572	Human Fetal Brain, normalized AC5002	Human Fetal Brain				pCMVSport 2.0
H0574	Hepatocellular Tumor; re-excision	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0575	Human Adult Pulmonary;re-excision	Human Adult Pulmonary	Lung			Uni-ZAP XR
H0576	Resting T-Cell; re- excision	T-Cells	Blood	Cell Line		Lambda ZAP II

Abdomen Abdomen Abdomen Human Pituitary Human Pituitary H.Leukocytes	Human Adult Heart;re- excision	eart;re-	Human Adult Heart	Heart		Uni-ZAP XR
human Pituitary Human Pituitar	lom 90 n	en 1in post	Abdomen		disease	pCMVSport 3.0
post Human PituitaryHuman PituitaryBreastdiseaseIst Human Primary Breast Cancer H.LeukocytesBreast A H.LeukocytesdiseaseA A H.LeukocytesCovary H.LeukocytesdiseaseA 	days	en post	Abdomen		disease	pCMVSport 3.0
Human Pituitary  H.Leukocytes  A H.Leukocytes	bdom &29 (	en lays post	Abdomen		disease	pCMVSport 3.0
y Breast         Human Primary Breast         Breast         disease           1sion         H.Leukocytes         H.Leukocytes         H.Leukocytes           150A3         H.Leukocytes         H.Leukocytes         H.Leukocytes           150 B         H.Leukocytes         H.Leukocytes         H.Leukocytes           15B         H.Leukocytes         disease           15B         Human Testes         Testis           15B         Human Adult Testis         Testis	ituitary	/, re-	Human Pituitary			pBluescript
H.Leukocytes         H.Leukocytes         H.Leukocytes           t, 500A         H.Leukocytes         H.Leukocytes           t, 500 B         H.Leukocytes         H.Leukocytes           t, 58B         H.Leukocytes         disease           t, 500 A         H.Leukocytes         disease           t, 500 A         H.Leukocytes         disease           t, 500 A         Ovarian Cancer         Ovary         disease           t, Breast         Human Testes         Testis         disease           ry Breast         Human Adult Testis         Testis         disease	rimary e-excisi	Breast	Human Primary Breast Cancer	Breast	disease	Uni-ZAP XR
H.Leukocytes H.Leukocytes H.Leukocytes H.Leukocytes H.Leukocytes H.Leukocytes Covarian Cancer Ovary Human Testes Testis Human Primary Breast Cancer Cancer Testis Human Adult Testis Testis	cytes,	50A3	H.Leukocytes			pCMVSport 1
H.Leukocytes H.Leukocytes H.Leukocytes Ovarian Cancer Human Primary Breast Cancer Human Adult Testis Human Adult Testis Human Adult Testis	ocytes,	> 500A	H.Leukocytes			pCMVSport 1
H.Leukocytes H.Leukocytes Ovarian Cancer Ovary Human Frimary Breast Cancer Human Adult Testis Human Adult Testis Festis Festis Festis	cocytes, zed cot :	500 B	H.Leukocytes			pCMVSport 1
H.Leukocytes Ovarian Cancer Ovary Human Testes Human Primary Breast Cancer Human Adult Testis Testis Festis	ocytes, ized cot	SB	H.Leukocytes			pCMVSport 1
Ovarian CancerOvarydiseaseHuman TestesTestisdiseaseHuman Primary BreastBreastdiseaseCancerTestisTestis	cocytes, zed cot	500 A	H.Leukocytes			pCMVSport 1
Human Primary Breast Breast disease  Human Adult Testis Testis	Ovarian Sion	Cancer	Ovarian Cancer	Ovary	disease	Uni-ZAP XR
Human Primary Breast Breast disease  Cancer  Human Adult Testis  Castis	Testes,		Human Testes	Testis		Uni-ZAP XR
Human Adult Testis Testis	Primary Reexcis	Breast ion	Human Primary Breast Cancer	Breast	disease	Uni-ZAP XR
Large Inserts, Reexcision	Adult T nserts, R	estes, eexcision	Human Adult Testis	Testis		Uni-ZAP XR

H0619	Fetal Heart	Human Fetal Heart	Heart			Uni-ZAP XR
H0620	Human Fetal Kidney;		Kidney			Uni-ZAP XR
H0622	Human Pancreas Tumor; Reexcision	Human Pancreas Tumor	Pancreas		disease	Uni-ZAP XR
H0623	Human Umbilical Vein; Reexcision	Human Umbilical Vein Endothelial Cells	Umbilical vein			Uni-ZAP XR
H0624	12 Week Early Stage Human II: Reexcision	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0625	Ku 812F Basophils Line	Ku 812F Basophils				pSport1
H0626	Saos2 Cells; Untreated	Saos2 Cell Line; Untreated				pSport1
H0627	Saos2 Cells; Vitamin D3 Treated				-	pSport1
Н0628	Human Pre- Differentiated	Human Pre-Differentiated Adipocytes				Uni-ZAP XR
	Adipocytes					
Н0629	Human Leukocyte, control #2	Human Normalized leukocyte				pCMVSport 1
H0631	Saos2, Dexamethosome	Saos2 Cell Line;				pSport1
	Treated	Dexamethosome I reated				
H0632	Hepatocellular Tumor;re- excision	Hepatocellular Tumor	Liver			Lambda ZAP II
Н0633	Lung Carcinoma A549	TNFalpha activated A549-			disease	pSport1
H0634	Human Testes Tumor,	Human Testes Tumor	Testis		disease	Uni-ZAP XR
	re-excision					
H0635	Human Activated T- Cells, re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0637	Dendritic Cells From CD34 Cells	Dentritic cells from CD34 cells				pSport1
Н0638	CD40 activated monocyte dendridic cells	CD40 activated monocyte dendridic cells				pSport1
H0640	Ficolled Human Stromal	Ficolled Human Stromal				Other
21221	I IVOIDA TRIBINI SE STIES			T		

	pSport1	Other	Other	Uni-ZAP XR	Uni-ZAP XR	pSport1		pSport1		pSport1		pSport1	pCMVSport 3.0	pSport1	pSport1	pSport1	Other
								disease		disease							
				Placenta	Heart												
Cells, Untreated	LPS activated monocyte derived dendritic cells	Hep G2 Cells	Hep G2 Cells	Human Placenta	Human Fetal Heart	Metastatic squamous cell lung carcinoma, poorly di		Invasive poorly differentiated lung adenocarcinoma		Papillary Cstic neoplasm of low malionant notentia		Normal Lung	B-Cells	Normal Ovary	Normal Lung	Stromal Cells	Metastatic Squamous cell lung Carcinoma poorly dif
Cells, Untreated	LPS activated derived dendritic cells	Hep G2 Cells, lambda library	Hep G2 Cells, PCR library	Human Placenta (re- excision)	Fetal Heart, re-excision	Lung, Cancer (4005313 A3): Invasive Poorly Differentiated Lung	Adenocarcinoma,	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma,	Metastatic	Ovary, Cancer: (4004562	Cystic Neoplasm, Low Malignant Pot	Lung, Normal: (4005313 B1)	B-Cells	Ovary, Normal: (9805C040R)	Lung, Normal: (4005313 B1)	Stromal Cells	Lung, Cancer: (4005313 A3) Invasive Poorly- differentiated Metastatic
į	H0641	H0642	H0643	H0644	H0645	H0646		H0647		H0648		H0649	H0650	H0651	H0652	H0653	H0654

	lung adenoc					
H0656	B-cells (unstimulated)	B-cells (unstimulated)				pSport1
H0657	B-cells (stimulated)	B-cells (stimulated)				pSport1
H0658	Ovary, Cancer (9809C332): Poorly	9809C332- Poorly differentiate	Ovary & Fallopian Tubes		disease	pSport1
	differentiated adenocarcinoma			_		
H0659	Ovary, Cancer	Grade II Papillary	Ovary		disease	pSport1
	(15395A1F): Grade II	Carcinoma, Ovary	•			•
	Papillary Carcinoma					
0990H	Ovary, Cancer:	Poorly differentiated			disease	pSport1
	(15799A1F) Poorly differentiated carcinoma	carcinoma, ovary				
H0661	Breast, Cancer: (4004943	Breast cancer			disease	pSport1
	A5)		,			
H0662	Breast, Normal:	Normal Breast -	Breast			pSport1
	(4005522B2)	#4005522(B2)				
H0663	Breast, Cancer: (4005522	Breast Cancer -	Breast		disease	pSport1
	A2)	#4005522(A2)				
H0664	Breast, Cancer: (9806C012R)	Breast Cancer	Breast		disease	pSport1
H0665	Stromal cells 3.88	Stromal cells 3.88				pSport1
9990H	Ovary, Cancer: (4004332	Ovarian Cancer, Sample			disease	pSport1
	A2)	#4004332A2				
L990H	Stromal cells(HBM3.18)	Stromal cell(HBM 3.18)				pSport1
8990H	stromal cell clone 2.5	stromal cell clone 2.5				pSport1
6990H	Breast, Cancer: (4005385 A2)	Breast Cancer (4005385A2)	Breast			pSport1
H0670	Ovary, Cancer(4004650	Ovarian Cancer -				pSport1 ·
	A3): Well-	4004650A3				-
	Differentiated					
	Micropapillary Serous Carcinoma					

pSport1	pSport1	Uni-ZAP XR	Uni-ZAP XR	pCMVSport 3.0	pCMVSport 3.0	PCRII	Other	pCMVSport 3.0	pCMVSport 3.0	pCMVSport 3.0	pCMVSport 3.0	pCMVSport 3.0	pCMVSport 3.0	pCMVSport 3.0
	Ovary	Prostate	Prostate				Placenta			Ovaries			Ovary	
Breast Cancer- Sample # 9802C02OE	Ovarian Cancer(4004576A8)	Human Prostate Cancer, stage B2	Human Prostate Cancer, stage C	Colon Cancer 9808C064R	Colon Cancer 9808C064R	B-Cells	Placenta	serous papillary adenocarcinoma (9606G304SPA3B)	Serous papillary adenocarcinoma, stage 3C (9804G01	Ovarian Cancer-9810G606	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-	Adenocarcinoma of Ovary, Human Cell Line, # SW-626	Human normal ovary(#9610G215)	Human Ovarian cancer(#9807G017),mRN
Breast, Cancer: (9802C02OE)	Ovary, Cancer: (4004576 A8)	Human Prostate Cancer, Stage B2; re-excision	Human Prostate Cancer, Stage C: re-excission	Colon, Cancer: (9808C064R)	Colon, Cancer: (9808C064R)-total RNA	TNFR degenerate oligo	screened clones from placental library	Serous Papillary Adenocarcinoma	Ovarian Serous Papillary Adenocarcinoma	Serous Papillary Adenocarcinoma	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3	Adenocarcinoma of Ovary, Human Cell Line	Human normal ovary(#9610G215)	Human Ovarian Cancer(#9807G017)
H0671	H0672	H0673	H0674	H0675	H0676	H0677	8290H	H0682	H0683	H0684	H0685	9890H	H0687	8890H

S0016	Kidney Pyramids	Kidney pyramids	Kidney			Uni-ZAP XR
S0021	Whole brain	Whole brain	Brain			ZAP Express
S0022	Human Osteoclastoma Stromal Cells -	Osteoclastoma Stromal Cells				Uni-ZAP XR
S0024	Human Kidney Medulla - unamplified	Human Kidney Medulla				
S0026	Stromal cell TF274	stromal cell	Bone marrow	Cell Line		Uni-ZAP XR
S0027	Smooth muscle, serum	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
	treated					
S0028	Smooth muscle, control	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0029	brain stem	Brain stem	brain			Uni-ZAP XR
S0030	Brain pons	Brain Pons	Brain			Uni-ZAP XR
S0031	Spinal cord	Spinal cord	spinal cord			Uni-ZAP XR
S0032	Smooth muscle-ILb induced	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0035	Brain medulla oblongata	Brain medulla oblongata	Brain			Uni-ZAP XR
S0036	Human Substantia Nigra	Human Substantia Nigra				Uni-ZAP XR
S0037	Smooth muscle, IL1b induced	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
80038	Human Whole Brain #2 - Oligo dT > 1.5Kb	Human Whole Brain #2				ZAP Express
80039	Hypothalamus	Hypothalamus	Brain			Uni-ZAP XR
S0040	Adipocytes	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0042	Testes	Human Testes				ZAP Express
S0044	Prostate BPH	prostate BPH	Prostate		disease	Uni-ZAP XR
S0045	Endothelial cells-control	Endothelial cell	endothelial cell- lung	Cell Line		Uni-ZAP XR
S0046	Endothelial-induced	Endothelial cell	endothelial cell- lung	Cell Line		Uni-ZAP XR
S0048	Human Hypothalamus, Alzheimer"s	Human Hypothalamus, Alzheimer"s			disease	Uni-ZAP XR

Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	pBluescript	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Lambda ZAP II	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	ZAP XR	
Uni-Z	Uni-2	Uni-2	Uni-2	Uni-ź	Uni-ź	Uni-,	Uni-2	Uni-	Uni-,	pBlu	Uni-	Uni-,	Uni-	Uni-,	Lam	Uni-,	Uni-	Uni-	Uni-	Uni-,	Uni-	41.5
	disease	disease			disease	disease				disease												
			Cell Line	Cell Line				Cell Line			Cell Line	Cell Line		Cell Line	Cell Line	Cell Line	Cell Line				Cell Line	
			poold	poold	BRAIN	Brain	Brain		Bone marrow	bone	Pulmanary artery	Knee			Bone marrow	lung	poold		Prostate	prostate	Prostate	A
Human Brain. Striatum	Human Frontal Cortex, Schizophrenia	Human Hypothalamus, Schizophrenia	human neutrophils	human neutrophil induced				Anergic T-cell	Bone marrow	Osteoclastoma	Smooth muscle	Osteoblasts	Airway Epithelial	apoptotic cells	stromal cell	eosinophil	macrophage-oxidized LDL treated	Macrophage (GM-CSF treated)	prostate BPH	Prostate	LNCAP Cell Line	
Himan Brain, Striatum	Human Frontal Cortex, Schizophrenia	Human Hypothalmus, Schizophre	neutrophils control	Neutrophils IL-1 and LPS induced	STRIATUM DEPRESSION	Brain Amygdala Depression	Hypothalamus	Anergic T-cell	Bone marrow	Osteoclastoma-	Smooth miscle-edited A	Osteoblasts	Epithelial-TNFa and INF induced	Apoptotic T-cell	PERM TF274	eosinophil-IL5 induced	Macrophage-oxLDL	Macrophage (GM-CSF	prostate-edited	Normal Prostate	LNCAP prostate cell line	
S0049	80050	S0051	S0052	S0053	S0106	S0110	S0112	S0114	S0116	S0122	20124	S0126	S0132	S0134	S0136	S0140	S0142	S0144	S0146	S0148	80150	, , ,

pBluescript	Uni-ZAP XR	Uni-ZAP XR	Uni-ZAP XR	pSport1	pSport1	pSport1	pSport1	pSport1	pBluescript	pSport1	pSport1	pSport1	Uni-ZAP XR		Uni-ZAP XR	Uni-ZAP XR	ZAP Express	Uni-ZAP XR		pSport1
		disease		disease		:							disease					disease		
									Cell Line						Cell Line	Cell Line				
	prostate								Pulmanary artery				9404	21100	poold		Brain	Brain		
PC3 prostate cell line	Prostate	Bone Marrow Stroma, TNF & LPS induced		Human Prostate BPH	Human Prostate BPH	Synovial Fibroblasts	Synovial Fibroblasts	Synovial Fibroblasts	Smooth muscle	Messangial cell	Messangial cell	Bone Marrow Stromal	Cell, untreated	Osteociastonia	human neutrophil induced	apoptotic cells	Hypothalamus	H. Brain, Frontal Cortex,	Epileptic	Camowiol Fibroblects
Prostate/LNCAP,	Prostate, normal,	Bone Marrow Stroma, TNF&LPS ind	Human B Cell 8866	Prostate, BPH, Lib 2	Prostate BPH, Lib 2, subtracted	Synovial Fibroblasts	Synovial hypoxia	Synovial IL-1/TNF stimulated	Smooth Muscle- HASTE normalized	Messangial cell, frac 1	Messangial cell, frac 2	Bone Marrow Stromal	Cell, untreated	Human Osteociastoma, re-excision	Neutrophils IL-1 and LPS induced	Apoptotic T-cell, re- excision	H. hypothalamus, frac	H. Frontal	cortex,epileptic;re- excision	Carried Dibushlanta
80168	S0176	S0180	S0182	S0188	80190	S0192	20104	96108	S0206	80208	\$0210	S0212	, , ,	S0214	S0216	S0218	S0220	S0222		0,000

S02-50         Human Osteoblasts II         Permat Cord, re-excision         Spinal cord         Spinal cord         Uni-ZAP XR           S02-76         Synovial Pypoxia-RSF         Synovial Phypoxia-RSF         Synovial Phypoxia-RSF         Uni-ZAP XR         Uni-ZAP XR           S02-78         Human Aplose Tissue, treated), re-excision         Human Aplose Tissue         Human Aplose Tissue         Uni-ZAP XR           re-excision         S02-8         Brain frontal cortex, re-		(III/TNF), subt				
Spinal Cord, re-excision         Spinal cord         spinal cord           Synovial hypoxia-RSF         Synovial fobroblasts         Synovial tissue           Synovial hypoxia-RSF         Macrophage (GM-CSF         Macrophage (GM-CSF           treated), re-excision         Human Adipose Tissue         Brain frontal cortex           Human Adipose Tissue, e-excision         Brain frontal cortex         Brain           excision         Osteoarthritic         Bone           Data part tumor         Larynx tumor         Larynx, vocal cord         disease           Larynx tumor         Larynx tumor         Larynx tumor         Larynx tumor           Larynx tumor         Larynx tumor         Larynx tumor         Larynx tumor           Larynx tumor         Larynx tumor         Larynx tumor         Larynx tumor           Excision         Genentia/Alzheiner*         Brain         disease           Excision         Larynx tumor         Larynx tumor         Larynx tumor           Excision         Larynx tumor         Larynx tumor         Larynx tumor           Spleen/fromal         Spleen normal         Spleen normal         Gertilage           Spleen/fromal         Human osteoarthritic         Larynx tumor         Human osteoarthritic           Aliman larchea         <	S0250	Human Osteoblasts II	Human Osteoblasts	Femur	disease	pCMVSport 2.0
Synovial hypoxia-RSF Synovial fobroblasts Synovial hypoxia-RSF (freumatoid)  H Macrophage (GM-CSF Macrophage (GM-CSF treated))  H Manan Adipose Tissue, Human Adipose Tissue  Brain Fontal Cortex, re- Brain frontal cortex  Brain Fontal Cortex, re- Cartilage  Larynx tumor Larynx tumor Larynx, vocal cord disease  Larynx tumor Bone marrow Bone marrow Bone marrow Stroma, treated Bone marrow Bone Brain Brain Bone Brain	S0260	Spinal Cord, re-excision	Spinal cord	spinal cord		Uni-ZAP XR
H Macrophage (GM-CSF treated)  Human Adipose Tissue, Human Adipose Tissue  Brain Frontal Cortex, re-excision  Osteoarthritis (OA-4)  Larynx tumor  Bone marrow  Stroma, treated  Frontal Lobe, dementia, redementia, redementi	S0276	Synovial hypoxia-RSF subtracted	Synovial fobroblasts (rheumatoid)	Synovial tissue		pSport1
Human Adipose Tissue, Human Adipose Tissue re-excision  Brain Frontal Cortex, re-excision Osteoarthritis (OA-4) Cartilage Laryux tumor Bone marrow Stroma, treated Excision Laryux normal #10 261- Laryux normal Normal trachea Human Normal Normal Cartilage Human Normal Human Normal Cartilage Human Normal Human Normal Cartilage Fraction II Palate carcinoma Palate carcinoma Palate carcinoma Palate normal Palate parynx carcinoma Palate normal Palate parynx carcinoma Parynx carcinoma Parynx carcinoma Parynx c	S0278	H Macrophage (GM-CSF	Macrophage (GM-CSF treated)			Uni-ZAP XR
Brain Frontal Cortex, re-excision         Brain frontal cortex         Brain Frontal Cortex, re-excision         Brain frontal cortex         Brain           Osteoarthritis (OA-4)         Human Osteoarthritic         Bone         disease           Larynx tumor         Larynx tumor         Larynx,vocal cord         disease           Bone marrow         Bone marrow         Bone marrow         Bone marrow           Stromat Leaded         Frontal Lobe         Brain         Brain           Earynx normal Marchea         Frontal Lobe         Brain         Brain           Spleen normal trachea         Normal trachea         Normal trachea         Normal trachea           Human         Human osteoarthritic         Cartilage         Brain           Human         Human osteoarthritic         Cartilage         Human Normal Cartilage           Human Normal Cartilage         Human Normal Cartilage         Human Normal Cartilage         Human Normal Cartilage           Fraction II         Palate carcinoma         Palate normal         Pharynx carcinom	S0280	Human Adipose Tissue, re-excision	Human Adipose Tissue			Uni-ZAP XR
Osteoarthritis (OA-4)         Human Osteoarthritic         Bone         disease           Larynx tumor         Larynx tumor         Larynx, vocal cord         disease           Bone marrow         Bone marrow         Bone marrow         Bone marrow           Stroma, treated         stroma, treatedSB         Brain         disease           Frontal Lobe         Brain         Brain         disease           Larynx normal #10 261         Larynx normal         Larynx normal         Larynx normal           Normal trachea         Normal trachea         Normal trachea         disease           Normal trachea         Normal trachea         Human osteoarthritic         disease           Atuman         eartilage         Human osteoarthritic         disease           Atuman Normal         Human Normal Cartilage         Human Normal Cartilage         Human Normal Cartilage           Fraction II         Palate carcinoma         Palate carcinoma         Divula           Palate carcinoma         Palate normal         Uvula           Pharynx carcinoma         Pharynx carcinoma         Pharynx carcinoma	S0282	Brain Frontal Cortex, re- excision	Brain frontal cortex	Brain		Lambda ZAP II
Larynx tumor         Larynx tumor         Larynx tumor         Larynx tumor         disease           Bone marrow         Bone marrow         Bone marrow         Bone marrow           stroma, treated         Frontal Lobe         Brain         Acmential           Frontal lobe, dementia, reacted SB         Brain         Brain           excision         Larynx normal         Acmentia/Alzheimer's         Acmential           Larynx normal #10 261-         Larynx normal         Spleen normal         Acmential           Spleen/normal         Spleen normal         Acmential         Acmential           Normal trachea         Normal trachea         Actilage         Actilage           Human Normal trachea         Human sosteoarthritic         Actilage           Human Normal Cartilage         Human Normal Cartilage         Actilage-Fraction I           Human Normal Cartilage         Human Normal Cartilage         Actilage-Fraction I           Human Normal Cartilage         Human Normal Cartilage         Actilage-Fraction I           Palate carcinoma         Palate normal         Alphopharynx	S0292	Osteoarthritis (OA-4)	Human Osteoarthritic Cartilage	Bone	disease	pSport1
Bone marrow         Bone marrow         Bone marrow           stroma,treated         stroma,treatedSB         Brain           Frontal Lobe         Brain         Brain           excision         Larynx normal         Larynx normal           1 arynx normal #10 261-         Larynx normal         Larynx normal           273         Spleen normal         Normal trachea           Normal trachea         Normal trachea         disease           Human         cartilage         disease           Human         cartilage         disease           Human Normal         Human Normal Cartilage         Human Normal Cartilage           Cartilage, Fraction I         Human Normal Cartilage         Human Normal Cartilage           Fraction II         Palate carcinoma         Uvula           Palate normal         Palate normal         Uvula           Pharynx carcinoma         Pharynx carcinoma         Hypopharynx	S0294	Larynx tumor	Larynx tumor	Larynx, vocal cord	disease	pSport1
Frontal lobe, dementia;re-         Frontal Lobe         Brain         Brain           excision         Larynx normal #10 261-         Larynx normal         Larynx normal #10 261-         Larynx normal           273         Spleen normal         Spleen normal         Abril	S0298	Bone marrow stroma treated	Bone marrow stroma, treatedSB	Bone marrow		pSport1
Larynx normal #10 261-Larynx normalLarynx normal273Spleen normalSpleen normalSpleen/normalSpleen normaldiseaseHumanHuman osteoarthriticdiseaseHumanCartilagediseaseHuman NormalCartilagediseaseHuman NormalHuman Normal CartilagediseaseHuman Normal CartilageHuman Normal CartilagediseaseFraction IIPalate carcinomaUvuladiseasePalate normalPalate normalUvuladiseasePharynx carcinomaPharynx carcinomaHypopharynxdisease	S0300	Frontal lobe, dementia; re- excision	Frontal Lobe dementia/Alzheimer"s	Brain		Uni-ZAP XR
Spleen/normal         Spleen normal           Normal trachea         Normal trachea           Human         Human osteoarthritic           Osteoarthritic;fraction II         Luman osteoarthritic           Human         Cartilage           Human Normal         Cartilage           Cartilage, Fraction I         Human Normal Cartilage           Human Normal Cartilage         Human Normal Cartilage           Fraction II         Palate carcinoma           Palate carcinoma         Uvula           Palate rormal         Palate normal           Pharynx carcinoma         Hypopharynx	S0306	Larynx normal #10 261- 273	Larynx normal			pSportl
Normal trachea         Normal trachea         Normal trachea           Human osteoarthritic osteoarthritic; fraction II         Human osteoarthritic         disease           Human Normal         cartilage         disease           Human Normal         Cartilage         disease           Cartilage, Fraction I         Human Normal Cartilage         disease           Fraction II         Palate carcinoma         Uvula         disease           Palate carcinoma         Palate normal         Uvula         disease           Pharynx carcinoma         Pharynx carcinoma         Hypopharynx         Hypopharynx	S0308	Spleen/normal	Spleen normal			pSport1
Human osteoarthritic;fraction IIHuman osteoarthritic cartilageHuman osteoarthritic cartilageHuman osteoarthritic cartilagediseaseHuman Normal Cartilage, Fraction IHuman Normal CartilageActilageHuman Normal Cartilage Fraction IIHuman Normal CartilageActilageFraction IIPalate carcinomaUvuladiseasePalate normalPalate normalUvuladiseasePharynx carcinomaPharynx carcinomaHypopharynxHypopharynx	S0310	Normal trachea	Normal trachea			pSport1
Human Osteoarthritic; fraction II cartilage  Human Normal Cartilage  Fraction II  Palate carcinoma  Palate carcinoma  Palate normal  Pharynx carcinoma  Pharynx carcinoma  Hypopharynx  Hypopharynx  Gisease  Hypopharynx  Hypopharynx  Gisease  Hypopharynx	S0312	Human	Human osteoarthritic		disease	pSport1
Osteoarthritis; fraction IcartilageHuman NormalCartilageCartilage, Fraction IHuman Normal CartilageFraction IIPalate carcinomaUvulaPalate normalPalate normalUvulaPharynx carcinomaHypopharynx	S0314	Osteoarumuc, iraction m Human	Human osteoarthritic		disease	pSport1
Cartilage, Fraction I         Human Normal Cartilage         Human Normal Cartilage         Adjust           Fraction II         Palate carcinoma         Uvula         disease           Palate normal         Palate normal         Uvula         Delate normal           Pharynx carcinoma         Pharynx carcinoma         Hypopharynx	S0316	osteoarthritis;fraction I Human Normal	Cartilage Human Normal Cartilage			pSport1
Palate carcinomaPalate carcinomaUvuladiseasePalate normalUvulaPharynx carcinomaHypopharynx	S0318	Cartilage, Fraction 1 Human Normal Cartilage Fraction II	Human Normal Cartilage			pSport1
Palate normalUvulaPharynx carcinomaHypopharynx	S0328	Palate carcinoma	Palate carcinoma	Uvula	disease	pSport1
Pharynx carcinoma Pharynx carcinoma Hypopharynx	S0330	Palate normal	Palate normal	Uvula		pSport1
	S0332	Pharynx carcinoma	Pharynx carcinoma	Hypopharynx		pSport1

S0334	Human Normal Cartilage	Human Normal Cartilage			·	pSport1	_
<del></del>	Human Normal Cartilage Fraction IV	Human Normal Cartilage				pSportl	
S0338	Human Osteoarthritic Cartilage Fraction III	Human osteoarthritic cartilage			disease	pSport1	
S0340	Human Osteoarthritic	Human osteoarthritic cartilage			disease	pSport1	
S0342	Adipocytes;re-excision	Human Adipocytes from Osteoclastoma				Uni-ZAP XR	
S0344	Macrophage-oxLDL; re-	macrophage-oxidized LDL	poold	Cell Line		Uni-ZAP XR	
S0346	Human Amygdala;re-	Amygdala				Uni-ZAP XR	
50278	Cheek Carcinoma	Cheek Carcinoma			disease	pSport1	
50350	Pharvnx Carcinoma	Pharynx carcinoma	Hypopharynx		disease	pSport1	
S0352	Larynx Carcinoma	Larynx carcinoma			disease	pSport1	
S0354	Colon Normal II	Colon Normal	Colon		•	pSport1	
S0356	Colon Carcinoma	Colon Carcinoma	Colon		disease	pSport1	
S0358	Colon Normal III	Colon Normal	Colon			pSport1	_
S0360	Colon Tumor II	Colon Tumor	Colon		disease	pSport1	_
S0362	Human Gastrocnemius	Gastrocnemius muscle				pSport1	_
S0364	Human Quadriceps	Quadriceps muscle				psport1	-
S0366	Human Soleus	Soleus Muscle				nSport1	
S0368	Human Pancreatic	Islets of Langerhans				moded	
T		1			disease	nSport1	Т
S0370	Larynx carcinoma II	Larynx carcinoma			disease	nSnort1	т
S0372	Larynx carcinoma III	Larynx carcinoma			Aceacin	nSnort1	т —
S0374	Normal colon	Normal colon			1:22.00	#C=0#1	_
S0376	Colon Tumor	Colon Tumor			disease	pspoliti	Т
S0378	Pancreas normal PCA4	Pancreas Normal PCA4				psporti	
ls	Pancreas Tumor PCA4	Pancreas Tumor PCA4 Tu			disease	pSport1	$\neg$
20200	Palicicas I union 1 COT						

S0428	Neutrophils control; re- excision	human neutrophils	poold	Cell Line		Uni-ZAP XR
S0430	Aryepiglottis Normal	Aryepiglottis Normal				pSport1
S0432	Sinus piniformis Tumour	Sinus piniformis Tumour				pSport1
S0434	Stomach Normal	Stomach Normal			disease	pSport1
S0436	Stomach Tumour	Stomach Tumour			disease	pSport1
S0438	Liver Normal Met5No	Liver Normal Met5No				pSport1
S0440	Liver Tumour Met 5 Tu	Liver Tumour				pSport1
S0442	Colon Normal	Colon Normal				pSport1
S0444	Colon Tumor	Colon Tumour			disease	pSport1
S0446	Tongue Tumour	Tongue Tumour				pSport1
S0448	Larynx Normal	Larynx Normal				pSport1
S0450	Larynx Tumour	Larynx Tumour				pSport1
S0452	Thymus	Thymus				pSport1
S0454	Placenta	Placenta	Placenta			pSport1
S0456	Tongue Normal	Tongue Normal				pSport1
S0458	Thyroid Normal (SDCA2	Thyroid normal				pSport1
	No)					
S0460	Thyroid Tumour	Thyroid Tumour				pSport1
S0462	Thyroid Thyroiditis	Thyroid Thyroiditis				pSport1
S0464	Larynx Normal	Larynx Normal				pSport1
S0466	Larynx Tumor	Larynx Tumor			disease	pSport1
S0468	Ea.hy.926 cell line	Ea.hy.926 cell line				pSport1
S0470	Adenocarcinoma	PYFD			disease	pSport1
S0472	Lung Mesothelium	PYBT				pSport1
S0474	Human blood platelets	Platelets	Blood platelets			Other
S990S	Human Amygdala; re-	Amygdala				Uni-ZAP XR
0.000	CACISSIOII	-	-			
S3012	Smooth Muscle Serum Treated, Norm	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S3014	Smooth muscle, serum induced,re-exc	Smooth muscle	Pulmanary artery	Cell Line		pBluescript

pBluescript SK-	pBluescript SK-	pBluescript SK-	pBluescript SK-	pAMP	pBluescript SK-	pBluescript SK-	pBluescript SK-		pBluescript SK-	, in the second	pBluescript SK-			pBluescript SK-		pBluescript SK-							
			disease	disease																			
												-											
Human Bone Marrow	Human Kidney, normal Adult	Human Adult Retina	Human Pancreatic Carcinoma																				
Human Bone Marrow	Human Kidney, normal Adult	Human Adult Retina	Human Pancreatic Carcinoma Screened	Alzheimer"s, exon tran.712P	Human colon carcinoma	HCC cell line metastisis	Human (HCC) cell line	liver (mouse) metastasis,	Human colon carcinoma	(HCC) cell line, remake	Human (Caco-2) cell	line, adenocarcinoma,	colon	Human (Caco-2) cell	line, adenocarcinoma,	Human Colon Carcinoma	Atrium cDNA library	Human heart	Clontech human aorta	polyA+ mRNA (#6572)	Human	Human adult (K.Okubo)	Human adult lung 3" directed Mbol cDNA
T0071 H	T	T0082 H		T0087 A	T0103 H	T0104 F	T0109 F		T0110 F	<u> </u>	T0112 F	_		T0114 F		T0115 F	L0002		T0002		L0015 I	L0021	L0022 1

																						1121	пега	HT1080		Patu 8988t	
																			brain		heart						liver
												amvedala	aorta		placenta	placenta		testis						fibrosarcoma		pancreatic cancer	
Human brain ARSanders	Human colon mucosa	Human epidermal	keratinocyte	Human keratinocyte differential display	(B.Lin)	Human pancreatic tumor	Human promyelocyte	Liver HepG2 cell line.	Subtracted human retina	Subtracted human retinal	pigment epithelium (RPF)	DKFZnhamv1	Human aorta polyA+	(TFujiwara)	Human placenta cDNA	Human placenta polyA+	(TFujiwara)	Human testis (C. De Smet)	Human fetal brain	(Trujiwara)	Human heart cDNA	(Y Nakamura)	Human HeLa (Y.Wang)	Human fibrosarcoma cell	line HT1080	Human pancreatic cancer cell line Patu 8988t	Human liver EST
L0024	L0040	L0041		L0045		L0053	L0055	T0065	9600T	L0097		1 0103	L0105		L0142	L0143		L0151	L0157		L0163		L0182	L0187		L0194	L0295

		BA, M13-derived	BA, M13-derived	Bluescript	Bluescript	Bluescript SK	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-
	E8CASS; variant of MCF7																						
						ovary								adrenal gland	brain	breast	colon	colon	colon	kidney	larynx	gunl	lymph node
	breast adenocarcinoma							germ cell tumor	germ cell tumor	pheochromocytoma	schizophrenic brain S-11 frontal lobe	Schwannoma tumor	synovial sarcoma	adrenal adenoma	pooled frontal lobe	breast tumor	colon tumor	tumor	tumor	kidney tumor	larynx	lung tumor	lymphoma
(Y.L.Yu)	Human E8CASS	Infant brain, Bento Soares	Normalized infant brain, Bento Soares	P, Human foetal Brain Whole tissue	S, Human foetal	Stratagene ovary (#937217)	Stratagene ovarian cancer (#937219)	NCI CGAP GC2	NCI CGAP GC5	NCI CGAP Phe1	Stratagene schizo brain	NCI CGAP Sch1	NCI CGAP SS1	NCI CGAP AA1	Johnston frontal cortex	NCI CGAP Br3	NCI CGAP Co12	NCI CGAP Col1	NCI CGAP Co2	NCI CGAP Kid6	NCI CGAP Larl	NCI CGAP Lu1	NCI CGAP Lym3
	L0309	L0351	L0352	L0355	L0356	L0361	L0362	1.0363	1.0364	L0365	T0366	1.0367	L0368	L0369	L0370	L0371	L0372	L0373	L0374	1.0375	1,0376	L0378	L0379

Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-	Bluescript SK-		Bluescript SK-	Bluescript SK-	Bluescript SK-	gt11		Lafmid A	Lafmid BA	Lafmid BA	Lafmid BA	Lafmid BA	lafmid BA	lafmid BA	Lafmid BA	Lafmid BK	lambda gt10	lambda gt10
pharynx	prostate	prostate	prostate	stomach	tongue		tonsil											brain	whole brain		eye	eye
squamous cell carcinoma	epithelium (cell line)	invasive tumor (cell line)	prostate tumor	gastric tumor	squamous cell carcinoma	from base of tongue	germinal center B-cells	normal gingiva (cell line from immortalized kerati	normal gingiva (cell line from primary keratinocyt									total brain			retina	retina
NCI CGAP HN4	NCI CGAP Pr25	NCI CGAP Pr24	NCI CGAP Pr23	NCI CGAP Gas1	NCI_CGAP_HN3		NCI CGAP GCB0	NCI_CGAP_HN6	NCI_CGAP_HNS	H, Human adult Brain	Cortex tissue	b4HB3MA Cot109+103+85-Bio	1-NIB	b4HB3MA Cot8-HAP-Ft	b4HB3MA-Cot109+10- Bio	Cot1374Ft-4HB3MA	Infant brain, LLNL array of Dr. M. Soares 1NIB	normalized infant brain cDNA	Soares infant brain 1NIB	N4HB3MK	Human retina cDNA randomly primed sublibrary	Human retina cDNA Tsp5091-cleaved sublibrary
L0381	L0382	L0383	L0384	L0385	L0386		_	L0388	L0389	L0394		L0404	L0411	L0415	L0418	L0428	L0435	L0438	L0439	L0446	L0455	L0456

lambda gt10	Lambda gt11	Lambda gt11	lambda gt11	lambda gt11	lambda nm1149	Lambda ZAP Express	Lambda Zap Express	(Stratagene)	Lalibua LAF II	Lambda ZAP, pBluescript SK(-)	Lambda ZAPII	Lambda ZAPII	Lambda ZAPII		pAMP	pAMP1	pAMP1	pAMP1		pAMPI	pAMP1	pAMP1	pAMP1
							KG1-a																
pooled				brain									leg muscle			ovary	bone marrow	bone marrow		bone marrow	brain	breast	breast
multi-tissue				brain									skeletal muscle			papillary serous carcinoma	+	CD34+, T negative,	myelogenou	stem cell 34+/38+	oligodendroglioma	adenocarcinoma	adenocarcinoma
multi-tissue normalized short-fragment	Adult heart, Clontech	Adult heart, Lambda gt 11	WATMI	fetal brain cDNA	TEST1, Human adult Testis tissue	Human fetal heart, Lambda ZAP Express	KG1-a Lambda Zap	Express cDNA library	retal brain, Stratagene	Stratagene cat#937212 (1992)	CD34+DIRECTIONAL	Human pancreatic islet	STRATAGENE Human	skeletal muscle cDNA library, cat. #936215.	Human Genomic	NCI CGAP Ov26	NCI_CGAP_HSC4	NCI_CGAP_HSC3		NCI CGAP HSC2	NCI CGAP Brn20	NCI CGAP Br15	NCI CGAP Br17
L0457	L0459	L0460	L0462	L0463	L0465	L0471	L0475	1.0476	L04/0	L0480	L0481	L0483	L0485		L0492	<del></del>	L0497	L0498		L0499	L0500	L0502	L0503

pAMP1	pAMP1	pAMP1	pAMP1	pAMP1		pAMP1	pAMP1		pAMP1		pAMP1	pAMP1	pAMP10	pAMP10	pAMP10	pAMP10		pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	pAMP10	<
breast	breast	breast	breast	gunl		lung	ovary		ovary		ovary	ovary																	•
breast carcinoma in situ	invasive carcinoma	lobullar carcinoma in situ	normal epithelium	bronchioalveolar	carcinoma	invasive adenocarcinoma	borderline ovarian	carcinoma	early stage papillary	serous carcinoma	papillary serous carcinoma	papillary serous carcinoma				alveolar	rhabdomyosarcoma	Ewing"s sarcoma	kidney	liposarcoma	liver	liver	metastatic prostate bone lesion	ovary	prostate	prostate	prostate	thyroid	
NCI CGAP Br13	NCI CGAP Br12	NCI CGAP Br16	NCI CGAP Br14	NCI_CGAP_Lu25		NCI CGAP Lu26	NCI_CGAP_Ov36		NCI_CGAP_Ov37		NCI CGAP 0v31	NCI_CGAP_Ov32	NCI CGAP Pr1	NCI CGAP Pr2	NCI CGAP Pr3	NCI_CGAP_Alv1		NCI CGAP Ew1	NCI CGAP Kid1	NCI CGAP Lip2	NCI CGAP Lil	NCI CGAP Li2	NCI_CGAP_Pr12	NCI CGAP Ov2	NCI CGAP Pr5	NCI CGAP Pr6	NCI CGAP Pr8	NCI_CGAP_Thy1	10011 6100 1014
L0504	$\vdash$	T0506	L0507	L0508	┰	_	L0512		L0513		L0514	L0515	L0517	L0518	-	L0520		L0521	L0522	L0523	L0524	L0525	L0526	L0527	+	L0529	L0530	L0532	1000

Brain cDNA Library				
Chromosome 7 Placental cDNA Library		placenta		pAMP10
NCI CGAP Pr10	invasive prostate tumor	prostate		pAMP10
NCI_CGAP_Pr11	normal prostatic epithelial cells	prostate		pAMP10
NCI_CGAP_Pr9	normal prostatic epithelial cells	prostate		pAMP10
NCI_CGAP_Pr4	prostatic intraepithelial neoplasia - high grade	prostate		pAMP10
L0545 NCI_CGAP_Pr4.1	prostatic intraepithelial neoplasia - high grade	prostate		pAMP10
NCI CGAP Pr18	stroma	prostate		pAMP10
NCI CGAP Pr16	tumor	prostate		pAMP10
NCI_CGAP_HN10	carcinoma in situ from retromolar trigone			pAMP10
NCI_CGAP_HN9	normal squamous epithelium from retromolar trigone			pAMP10
NCI_CGAP_HN7	normal squamous epithelium, floor of mouth			pAMP10
NCI CGAP Co22	colonic adenocarcinoma	colon		pAMP10
NCI CGAP Li8		liver		pAMP10
NCI_CGAP_Ov40	endometrioid ovarian metastasis	ovary		pAMP10
NCI_CGAP_Ov39	papillary serous ovarian metastasis	ovary		pAMP10
NCI_CGAP_HN12	moderate to poorly differentiated invasive carcino	tongue		pAMP10
NCI_CGAP_HN11	normal squamous epithelium	tongue		pAMP10
Chromosome 7 HeLa			HeLa cell line;	pAMP10

	pBluescript	pBluescript	pBluescript SK	pBluescript SK(+)	pBluescript SK(-)	pBluescript SK-		pBluescript SK-	pBluescript SK- pBluescript SK-	pBluescript SK- pBluescript SK- pBluescript SK-	pBluescript SK- pBluescript SK- pBluescript SK- pBluescript SK-	pBluescript SK- pBluescript SK- pBluescript SK- pBluescript SK- pBluescript SK-	pBluescript SK-	pBluescript SK-	pBluescript SK-	pBluescript SK-
		Hip	liver												brain	brain
	bone marrow stroma	Bone													neuroepithelial cells	neuroepithelial cells
cDNA Library	Jia bone marrow stroma	Normal Human Trabecular Bone Cells	Stratagene liver (#937224)	Stratagene cDNA library Human heart, cat#936208	HTCDL1	Stratagene colon HT29 (#937221)		tratagene endothelial ell 937223	Stratagene endothelial cell 937223 Stratagene fetal retina 937202	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212)	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216 Stratagene hNT neuron (#937233)	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216 Stratagene hNT neuron (#937233) Stratagene neuroepithelium (#937231)	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216 Stratagene hNT neuron (#937233) Stratagene neuroepithelium (#937231) Stratagene neuroepithelium (#937231) Stratagene neuroepithelium	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216 Stratagene hNT neuron (#937233) Stratagene neuroepithelium (#937231) Stratagene neuroepithelium NT2RAMI 937234 Stratagene neuroepithelium	Stratagene endothelial cell 937223 Stratagene fetal retina 937202 Stratagene fibroblast (#937212) Stratagene HeLa cell s3 937216 Stratagene hNT neuron (#937231) Stratagene neuroepithelium (#937231) Stratagene neuroepithelium NT2RAMI 937234 Stratagene NT2 neuronal precursor 937230 Stratagene ONT2 neuronal Stratagene NT2 neuronal precursor 937230 Stratagene colon (#937204)
3	L0564 J	L0565 N	() S 18507	L0584 S	L0586 F	L0587 S	┝	C T0588 C		<del></del>				<del></del>	<del></del>	<del></del>

	stroma (#937222)				
L0598	Morton Fetal Cochlea	cochlea	ear		pBluescript SK-
L0599	Stratagene lung (#937210)		lung		pBluescript SK-
T0600	Weizmann Olfactory Epithelium	olfactory epithelium	nose		pBluescript SK-
L0601	Stratagene pancreas (#937208)		pancreas		pBluescript SK-
L0602	Pancreatic Islet	pancreatic islet	pancreas		pBluescript SK-
F0903	Stratagene placenta (#937225)		placenta		pBluescript SK-
L0604	Stratagene muscle 937209	muscle	skeletal muscle		pBluescript SK-
T0605	Stratagene fetal spleen (#937205)	fetal spleen	spleen		pBluescript SK-
F0000	NCI CGAP Lym5	follicular lymphoma	lymph node		pBluescript SK-
L0607	NCI CGAP Lym6	mantle cell lymphoma	lymph node		pBluescript SK-
T0608	Stratagene lung carcinoma 937218	lung carcinoma	lung	NCI-H69	pBluescript SK-
F0609	Schiller astrocytoma	astrocytoma	brain		pBluescript SK- (Stratagene)
L0610	Schiller glioblastoma multiforme	glioblastoma multiforme	brain		pBluescript SK- (Stratagene)
L0611	Schiller meningioma	meningioma	brain		pBluescript SK- (Stratagene)
L0612	Schiller oligodendroglioma	oligodendroglioma	brain		pBluescript SK- (Stratagene)
L0615	22 week old human fetal liver cDNA library				pBluescriptII SK(-)
T0619	Chromosome 9 exon II				pBluescriptIIKS+
L0622	HM1				pcDNAII (Invitrogen)
L0623	НМЗ	pectoral muscle (after mastectomy)			pcDNAII (Invitrogen)

L0625	NCI CGAP ARI	bulk alveolar tumor		pCMV-SPORT2
L0626	NCI CGAP GC1	bulk germ cell seminoma		pCMV-SPORT2
L0627	NCI CGAP Co1	bulk tumor	colon	pCMV-SPORT2
	NCI CGAP Ov1	ovary bulk tumor	ovary	pCMV-SPORT2
L0629	NCI_CGAP_Mel3	metastatic melanoma to	bowel (skin	pCMV-SPORT4
		bowel	primary)	
L0630	NCI CGAP CNS1	substantia nigra	brain	pCMV-SPORT4
L0631	NCI CGAP Br7		breast	pCMV-SPORT4
L0634	NCI CGAP Ov8	serous adenocarcinoma	ovary	pCMV-SPORT4
L0635	NCI_CGAP_PNS1	dorsal root ganglion	peripheral nervous system	pCMV-SPORT4
L0636	L0636 NCI_CGAP_Pit1	four pooled pituitary adenomas	brain	pCMV-SPORT6
L0637	NCI CGAP Brn53	three pooled meningiomas	brain	pCMV-SPORT6
T0638	NCI_CGAP_Brn35	tumor, 5 pooled (see description)	brain	pCMV-SPORT6
L0639	NCI_CGAP_Bm52	tumor, 5 pooled (see description)	brain	pCMV-SPORT6
L0640	NCI_CGAP_Br18	four pooled high-grade tumors, including two prima	breast	pCMV-SPORT6
L0641	NCI CGAP Co17	juvenile granulosa tumor	colon	pCMV-SPORT6
L0642	NCI_CGAP_Co18	moderately differentiated adenocarcinoma	colon	pCMV-SPORT6
L0643	NCI_CGAP_Co19	moderately differentiated adenocarcinoma	colon	pCMV-SPORT6
L0644	NCI_CGAP_Co20	moderately differentiated adenocarcinoma	colon	pCMV-SPORT6
L0645	NCI_CGAP_Co21	moderately differentiated adenocarcinoma	colon	pCMV-SPORT6
L0646	L0646 NCI_CGAP_Co14	moderately-differentiated adenocarcinoma	colon	pCMV-SPORT6
L0647	NCI CGAP Sar4	five pooled sarcomas,	connective tissue	pCMV-SPORT6

	pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6	VE TO SEE	pCMV-SPORT6	pCMV-SPORT6		pCMV-SPORT6	H 4 ( ) 4 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 ( ) 1 (	pCMV-SPORT6	pCMV-SPORT6		pCMV-SPORT6	pCMV-SPORT6		pCMV-SPORT6		pCMV-SPORT6	pCMV-SPORT6	TOOLS WAY	pciviv-sporto		pCMV-SPORT6	pCMV-SPORT6	
	esophagus	genitourinary tract	kidney		kidney	lung	!	gun		lung, cell line	lymph node		ovary	ovary		ovary		pancreas	skin	1	stomacn		uterus	uterus	
including myxoid liposarcoma	squamous cell carcinoma	2 pooled high-grade transitional cell tumors	2 pooled Wilms" tumors, one primary and one	metast	renal cell tumor	four pooled poorly- differentiated	adenocarcinomas	two pooled squamous cell	Calcillomas		lymphoma, follicular	mixed small and large cell	normal epithelium	tumor, 5 pooled (see	description)	tumor, 5 pooled (see	description)	adenocarcinoma	malignant melanoma,	metastatic to lymph node	poorly differentiated	adenocarcinoma with signet r	moderately-differentiated endometrial adenocarcino	poorly-differentiated	adenocarcinoma,
	NCI CGAP Eso2	NCI_CGAP_GUI	NCI_CGAP_Kid13		NCI CGAP Kid8	NCI_CGAP_Lu27		NCI_CGAP_Lu28		NCI CGAP Lu31	NCI_CGAP_Lym12		NCI CGAP Ov38	NCI_CGAP_Ov23		L0658 NCI_CGAP_Ov35		NCI CGAP Pan1	NCI_CGAP_Mel15	A CONTRACTOR	NCI_CGAP_Gas4		NCI_CGAP_Ut2	NCI_CGAP_Ut3	
	L0648	L0649	T0650			L0652		L0653	-+	L0654	T0655		T0656	L0657		T0658		F0659	L0661	_	79907		F0993	L0664	

pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6	pCR2.1-TOPO (Invitrogen)	pCRII	PGEM 5zf(+)	PGEM 5zf(+)	pOTB7	pOTB7	pOTB7	pSPORT1	pT7T3-Pac	pT7T3D	pT7T3D (Pharmacia) with a modified polylinker	pT7T3D (Pharmacia) with a modified polylinker	pT7T3D (Pharmacia) with a modified polylinker	pT7T3D (Pharmacia) with a modified
									MGC3							
uterus	uterus	whole blood	brain				muscle	placenta	lung		uterus			brain	brain	breast
serous papillary carcinoma, high grade, 2 pooled t	well-differentiated endometrial adenocarcinoma, 7	myeloid cells, 18 pooled CML cases, BCR/ABL rearra	frontal lobe (see description)				rhabdomyosarcoma	choriocarcinoma	small cell carcinoma				melanocyte			
L0665 NCI_CGAP_Ut4	NCI_CGAP_Ut1	NCI_CGAP_CML1	Stanley Frontal SN pool	Testis, Subtracted	Testis 1	Testis 2	NIH MGC 17	NIH MGC 21	NIH MGC 7	Gessler Wilms tumor	Soares_pregnant_uterus_ NbHPU	Human colorectal cancer	Soares melanocyte 2NbHM	Soares adult brain N2b4HB55Y	Soares adult brain N2b5HB55Y	Soares breast 2NbHBst
T0665	T0666	L0667	70686	0690T	L0697	8690T	T0708	T0709	L0710	L0717	L0731	L0738	L0740	L0741	L0742	L0743

L0745 Soal				 
<del></del>			_	with a modified
<del></del>				polylinker
	Soares retina N2b4HR	retina	eye	pT7T3D (Pharmacia)
_+				with a modified
				polylinker.
	Soares retina N2b5HR	retina	eye	pT7T3D (Pharmacia)
				 with a modified
				polylinker
L0747 Soa	Soares_fetal_heart_NbH		heart	pT7T3D (Pharmacia)
H19W				 with a modified
				polylinker
L0748   Soal	Soares fetal liver spleen		Liver and Spleen	pT7T3D (Pharmacia)
Z Z	INFLS			 with a modified
				polylinker
L0749   Soal	Soares_fetal_liver_splee		Liver and Spleen	pT7T3D (Pharmacia)
n_1	n_INFLS_S1			 with a modified
				polylinker
L0750   Soai	Soares_fetal_lung_NbHL		gunl	 pT7T3D (Pharmacia)
V61	· ·			with a modified
				polylinker
L0751   Soal	Soares ovary tumor	ovarian tumor	ovary	pT7T3D (Pharmacia)
IqN —	NeHOT			 with a modified
				polylinker
L0752   Soal	Soares_parathyroid_tum	parathyroid tumor	parathyroid gland	pT7T3D (Pharmacia)
orl	or_NbHPA			with a modified
				polylinker
L0753 Soa	Soares pineal gland N3		pineal gland	pT7T3D (Pharmacia)
HPG	Ü			with a modified
				polylinker
L0754   Soa	Soares placenta Nb2HP		placenta	pT7T3D (Pharmacia)
				with a modified
ļ				polylinker

pT7T3D (Pharmacia) with a modified polylinker	pT7T3D (Pharmacia) with a modified polylinker V TYPE	pT7T3D (Pharmacia) with a modified polylinker V TYPE	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker
placenta								·		
	multiple sclerosis lesions	senescent fibroblast			aorta	B-cell, chronic lymphotic leukemia	breast	breast	colon	colon
Soares_placenta_8to9we eks_2NbHP8to9W	Soares_multiple_sclerosi s_2NbHMSP	Soares senescent fibrobl asts_NbHSF	Soares_testis_NHT	Soares_total_fetus_Nb2 HF8_9w	Barstead aorta HPLRB3	NCI_CGAP_CLL1	NCI_CGAP_Br1.1	NCI_CGAP_Br2	NCI_CGAP_Co3	NCI_CGAP_Co4
L0755	L0756	L0757	L0758	L0759	T0760	L0761	L0762	L0763	L0764	L0765

							<del></del>			
pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modiffed polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modiffed polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker			
			brain	brain	colon	colon	colon	kidney	kidney	gunl
germinal center B cell	pooled germ cell tumors	pooled germ cell tumors	anaplastic oligodendroglioma	glioblastoma (pooled)	adenocarcinoma	colon tumor RER+	colon tumor RER+		2 pooled tumors (clear cell type)	carcinoid
L0766 NCI_CGAP_GCB1	NCI_CGAP_GC3	NCI_CGAP_GC4	NCI_CGAP_Bm25	NCI_CGAP_Bm23	NCI_CGAP_Co8	NCI_CGAP_Co10	NCI_CGAP_Co9	NCI_CGAP_Kid3	NCI_CGAP_Kid5	NCI_CGAP_Lu5
L0766	L0767	L0768	69L0T	L0770	L0771	L0772	L0773	L0774	L0775	L0776

pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT/T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT/T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a	modified polylinker
mixed (see below)	pancreas	polood	palood	prostate	prostate	soft tissue	spleen	whole brain		
Pooled human melanocyte, m fetal heart, and pregnant				normal prostate	normal prostate	leiomyosarcoma				_
L0777 Soares_NhHMPu_S1	Barstead pancreas HPLRB1	Soares_NFL_T_GBC_S1	Soares_NSF_F8_9W_O T_PA_P_S1	NCI_CGAP_Pr21	NCI_CGAP_Pr22	NCI_CGAP_Lei2	Barstead spleen HPLRB2	Soares_NbHFB	NCI_CGAP_Sub1	
L0777	F0778	L0779	L0780	L0782	L0783	L0784	L0785	T0786	L0787	

pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker							
						brain	colon	kidney	kidney	lung
					pooled germ cell tumors	medulloblastoma	colon tumor, RER+		2 pooled tumors (clear cell type)	carcinoid
NCI_CGAP_Sub3	NCI_CGAP_Sub4	NCI_CGAP_Sub5	NCI_CGAP_Sub6	NCI_CGAP_Sub7	NCI_CGAP_GC6	NCI_CGAP_Brm50	NCI_CGAP_Co16	NCI_CGAP_Kid11	NCI_CGAP_Kid12	NCI_CGAP_Lu24
L0789	T0790	L0791	L0792	L0793	L0794	F0796	L0800	L0803	L0804	L0805

pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	pT7T3D-Pac (Pharmacia) with a modified polylinker	puc18	puc18	puc18	puc18	puc18	puc18			pBluescript sk(-)	pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6						
																		:				
lung	ovary	prostate	prostate	breast	breast	breast	colon	colon	colon	head_neck	head neck	head_neck	head_neck	stomach	stomach				colon	eye	gunl	gunl
squamous cell carcinoma, poorly differentiated (4	fibrotheoma															Fetal lung	placenta	corresponding non cancerous liver tissue	adenocarcinoma	retinoblastoma	large cell carcinoma	large cell carcinoma, undifferentiated
L0806 NCI_CGAP_Lu19	NCI_CGAP_Ov18	Barstead prostate BPH HPLRB4 1	NCI_CGAP_Pr28	BT0254	BT0333	BT0559	CT0249	CT0254	CT0322	HT0229	HT0268	HT0340	HT0342	ST0186	ST0240	Human fetal lung	Human placenta	GLC	NIH MGC 65	NIH MGC 67	NIH MGC 68	NIH_MGC_69
F0806	L0807	F0808	F0809	F0879	L0946	L1057	L1441	L1446	L1499	L1788	L1819	L1877	L1878	L2138	L2174	L2251	L2252	L2255	L2257	L2258	L2259	L2260

L2261 NIH MGC 70	epithelioid carcinoma	pancreas	pCMV-SPORT6	PORT6
NIH MGC 72	melanotic melanoma	skin	pCMV-SPORT6	PORT6
NIH MGC 66	adenocarcinoma	ovary	pCMV-SI	PORT6
NIH MGC 71	leiomyosarcoma	uterus	pCMV-SPORT6	PORT6
NIH MGC 39	adenocarcinoma	pancreas	pOTB7	
Lupski_dorsal_root_gang	dorsal root ganglia		S-VMV-SI	pCMV-SPORT6 (Life
lion			Technolo	gies)
BT0757		breast	puc18	
CT0417		colon	puc18	
CT0432		colon	puc18	
CT0483		colon	puc18	!
UT0021		uterus tumor	puc18	
UT0039		uterus_tumor	puc18	
NN0054		nervous normal	puc18	
NN0068	•	nervous normal	puc18	
NN0116		nervous normal	puc18	
NN0136	-	nervous normal	puc18	
NN0141		nervous normal	puc18	
NN1022		nervous normal	puc18	
NN1023		nervous normal	puc18	
HT0559		head neck	puc18	
HT0594		head neck	puc18	
HT0618		head_neck	puc18	
HT0636		head neck	puc18	
HT0697		head_neck	puc18	
HT0698		head neck	puc18	
HT0704		head_neck	puc18	
HT0727		head_neck	puc18	
HT0728		head neck	puc18	
HT0734		head_neck	puc18	
HT0743		head neck	puc18	
HT0771		head neck	puc18	

L2598	HT0809		head neck	puc18
L2634	HT0872		head neck	puc18
L2637	HT0877		head_neck	puc18
L2640	HT0881		head neck	puc18
L2647	HT0894		head neck	puc18
L2650	HT0934		head neck	puc18
L2651	NIH MGC 20	melanotic melanoma	skin	pOTB7
L2653	NIH MGC 58	hypernephroma	kidney	pDNR-LIB (Clontech)
L2654	NIH MGC 9	adenocarcinoma cell line	ovary	pOTB7
L2655	NIH_MGC_55	from acute myelogenous leukemia	bone marrow	pDNR-LIB (Clontech)
L2657	NIH_MGC_54	from chronic myelogenous leukemia	bone marrow	pDNR-LIB (Clontech)
L2667	NT0013		nervous tumor	puc18
L2669	NT0022		nervous tumor	puc18
L2670	NT0023		nervous tumor	puc18
L2671	NT0024		nervous tumor	puc18
L2677	NT0039		nervous tumor	puc18
T7686	NT0058		nervous tumor	puc18
L2702	NT0098		nervous tumor	puc18
-	NT0104		nervous tumor	puc18
	NT0105		nervous tumor	puc18
L2716	NT0117		nervous tumor	puc18
L2738	GN0049		placenta normal	puc18
	FT0044		prostate tumor	puc18
L2791	FT0077		prostate_tumor	puc18
L2799	FT0096		prostate_tumor	puc18
L2804	FT0103		prostate_tumor	puc18
L2817	FT0131		prostate tumor	puc18
L2831	FT0162		prostate tumor	puc18
L2842	UM0009		uterus	puc18
L2852	UM0077		uterus	puc18

puc18	puc 1 8	puc18	puc18	puc18	puc18	puc18	nic18	810110	01000	puc18	puc10	pució	pució	pució	buc18	puc18	puc18	puc18	puc18	puc18												
amnion normal	amnion normal	amnion normal	breast normal	lung normal	ling tumor	ling timor	ling timor	Iulig tulifor	lung tumor	lung tumor	lung tumor	lung tumor	marrow	marrow	ovary	ovary	ovary	ovary	ovarv	Ovarv	prostate normal											
L2865 AN0004	十	+	+	-	+	+	+		L2913 BIN0090	+	+	╁	+	+-	+	$\neg$	+	+	L3111 ET0058	L3117 ET0068	L3118 ET0070	L3119 ET0072	L3127 ET0084	╁	1	+-	┿	+	+	+	+	1326 FN0019

puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	pBluescript sk(-)	pBluescript sk(-)	pDNR-LIB (Clontech)	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18	puc18
prostate normal	prostate normal	prostate normal	prostate normal	stomach normal	stomach normal	testis normal			bladder	amnion normal	amnion normal	breast	colon	colon	colon	prostate tumor	placenta normal	placenta normal	placenta_normal	placenta normal	placenta normal	head neck									
											hepatocellular carcinoma	hepatocellular carcinoma	carcinoma, cell line																		
1,3262   FN0073	╀╌	+	╁	+-	+-	+	+-	+	+	1-	L3387 GKB	L3388 GKC	+	AN0086	+	$\top$	╁	+	╀	_	┪┈╴	+	+	1	+-	+	+	╅╴	+	+-	+-

L3516   H	HT0913		head neck	puc18
L3518 F	HT0915		head neck	puc18
L3521 H	HT0919		head neck	puc18
	HT0939		head_neck	puc18
L3561 T	TN0025		testis_normal	puc18
L3562 T	TN0030		testis normal	puc18
T3603 L	UM0093		uterus	puc18
L3618 L	UT0050		uterus tumor	puc18
L3632 L	UT0074		uterus tumor	puc18
L3642 A	ADA	Adrenal gland		pBluescript sk(-)
L3643 A	ADB	Adrenal gland		pBluescript sk(-)
L3644 A	ADC	Adrenal gland		pBluescript sk(-)
L3645 C	Cu	adrenal cortico adenoma for Cushing's syndrome		pBluescript sk(-)
L3646 D	DCA			pTriplEx2
L3649   E	DCB	!		pTriplEx2
L3653   F	HTB	Hypothalamus		pBluescript sk(-)
_	HTC	Hypothalamus		pBluescript sk(-)
L3657 F	HTF	Hypothalamus		pBluescript sk(-)
L3658 c	cdA	pheochromocytoma		pTriplEx2
L3659 C	CB	cord blood		pBluescript
	NPA	pituitary		pBluescript sk(-)
L3665 N	NIH MGC 75		kidney	pDNR-LIB (Clontech)
L3667 N	NIH MGC 79		placenta	pDNR-LIB (Clontech)
$\neg$	AN0084		amnion normal	puc18
L3684 B	BT0812		breast	puc18
L3705 C	CT0486		colon	puc18
	GN0079		placenta normal	puc18
	HT0916		head neck	puc18
L3750 E	HT0945		head neck	puc18
$\dashv$	TN0136		testis normal	puc18
L3807 L	UT0077		uterus tumor	puc18

puc18	pBluescript sk(-)	pBluescript sk(-)	pTriplEx2	pTriplEx2	pTriplEx2	pME18SFL3	pME18SFL3	pDNR-LIB (Clontech)	pME18SFL3	pME18SFL3	pUC19FL3	pME18SFL3	pME18SFL3	pME18SFL3	pME18SFL3	pME18SFL3	pME18SFL3	pME18SFL3	pOTB7	pOTB7	pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6	pCMV-SPORT6
									NT2	NT2	NT2	NT2	NT2	NT2										
uterus tumor								liver											lung	brain	skin, normal, 4 pooled sa	brain	brain	, breast
	pituitary	pituitary	pituitary tumor	Bone marrow	Bone marrow	whole embryo, mainly head	whole embryo, mainly body								ovary, tumor tissue	placenta	placenta	thyroid gland	large cell carcinoma	neuroblastoma		glioblastoma with EGFR amplification	anaplastic oligodendroglioma with	invasive ductal carcinoma, 3 pooled samples
UT0078	NPC	NPD	TP	BM	MDS	HEMBAI	HEMBB1	NIH MGC 76		NT2RM4	NT2RP1	NT2RP2	NT2RP3	NT2RP4	OVARC1	PLACE1	PLACE3	THYROI	NIH MGC 18	NIH MGC 19	NCI_CGAP_Skn1	NCI_CGAP_Bm64	NCI_CGAP_Brn67	NCI_CGAP_Br22
13808	L3811		+-	+			L3817	1.3819	13824	1.3825	1.3826	1.3827	1.3828	1,3829	1,3831	L3832	L3834	L3837	L3841	L3871		L3904	L3905	L4497

L4501	L4501 NCI CGAP Sub8			pT7T3D-Pac
	i I			(Pharmacia) with a
				modified polylinker
L4537	NCI_CGAP_Thy7	follicular adenoma (benign lesion)	thyroid	pAMP10
L4556	NCI CGAP HN13	squamous cell carcinoma	tongue	pCMV-SPORT6
L4558	L4558 NCI CGAP Pan3		pancreas	pCMV-SPORT6
L4560	NCI CGAP Ut7	tumor	uterus	pCMV-SPORT6
L4669	L4669 NCI CGAP Ov41	serous papillary tumor	ovary	pCMV-SPORT6
L4747	L4747 NCI_CGAP_Bm41	oligodendroglioma	brain	pT7T3D-Pac
				 (Pharmacia) with a
				modified polylinker
L5286	NCI_CGAP_Thy10	medullary carcinoma	thyroid	pAMP10
L5564	L5564 NCI_CGAP_HN20		normal head/neck tissue	pAMP1
L5565	NCI_CGAP_Brn66	glioblastoma with	brain	pCMV-SPORT6
	ı	probably TP53 mutation		
		and witho		
T2566	NCI_CGAP_Brn70	anaplastic	brain	pCMV-SPORT6.ccdb
		oligodendroglioma		
L5568	NCI CGAP HN21	nasopharyngeal carcinoma	head/neck	pAMP1
L5569	NCI CGAP HN17	normal epithelium	nasopharynx	pAMP10
L5574	LSS74 NCI CGAP HN19	normal epithelium	nasopharynx	pAMP10
L5575	L5575 NCI_CGAP_Bm65	glioblastoma without	brain	pCMV-SPORT6
		EGFR amplification		
L5622	NCI CGAP Skn3		skin	pCMV-SPORT6
L5623	NCI CGAP Skn4	squamous cell carcinoma	skin	pCMV-SPORT6

## **Description of Table 5**

Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1B.1, column 9. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). Column 2 provides diseases associated with the cytologic band disclosed in Table 1B.1, column 8, as determined using the Morbid Map database.

Table 5

5

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OMIM Reference	Description
100690	Myasthenic syndrome, slow-channel congenital, 601462
100710	Myasthenic syndrome, slow-channel congenital, 601462
101000	Meningioma, NF2-related, sporadic Schwannoma, sporadic
101000	Neurofibromatosis, type 2
101000	Neurolemmomatosis
101000	Malignant mesothelioma, sporadic
102578	Leukemia, acute promyelocytic, PML/RARA type
102770	Myoadenylate deaminase deficiency
103050	Autism, succinylpurinemic
103050	Adenylosuccinase deficiency
103850	Aldolase A deficiency
104770	Amyloidosis, secondary, susceptibility to
106100	Angioedema, hereditary
106150	Hypertension, essential, susceptibility to
106150	Preeclampsia, susceptibility to
106165	Hypertension, essential, 145500
106180	Myocardial infarction, susceptibility to
107300	Antithrombin III deficiency
107670	Apolipoprotein A-II deficiency
107741	Hyperlipoproteinemia, type III
107777	Diabetes insipidus, nephrogenic, autosomal recessive, 222000
108725	Atherosclerosis, susceptibility to
108985	Atrophia areata
109270	Renal tubular acidosis, distal, 179800
109270	Spherocytosis, hereditary
109270	[Acanthocytosis, one form]
109270	[Elliptocytosis, Malaysian-Melanesian type]
109270	Hemolytic anemia due to band 3 defect
109560	Leukemia/lymphoma, B-cell, 3
109690	Asthma, nocturnal, susceptibility to
109690	Obesity, susceptibility to
109700	Hemodialysis-related amyloidosis
110100	Blepharophimosis, epicanthus inversus, and ptosis, type 1
110700	Vivax malaria, susceptibility to
113100	Brachydactyly, type C

112000	Hearthlade managing familial time I
113900	Heart block, progressive familial, type I
114835	Monocyte carboxyesterase deficiency
115665	Cataract, congenital, Volkmann type
116800	Cataract, Marner type
116806	Colorectal cancer
116860	Cavernous angiomatous malformations
117700	[Hypoceruloplasminemia, hereditary]
117700	Hemosiderosis, systemic, due to aceruloplasminemia
118485	Polycystic ovary syndrome with hyperandrogenemia
118800	Choreoathetosis, familial paroxysmal
120070	Alport syndrome, autosomal recessive, 203780
120131	Alport syndrome, autosomal recessive, 203780
120131	Hematuria, familial benign
120140	Osteoarthrosis, precocious
120140	SED congenita
120140	SMED Strudwick type
120140	Stickler syndrome, type I
120140	Wagner syndrome, type II
120140	Achondrogenesis-hypochondrogenesis, type II
120140	Kniest dysplasia
120150	Osteogenesis imperfecta, 4 clinical forms, 166200, 166210,
	259420, 166220
120150	Osteoporosis, idiopathic, 166710
120150	Ehlers-Danlos syndrome, type VIIA1, 130060
120215	Ehlers-Danlos syndrome, type I, 130000
120215	Ehlers-Danlos syndrome, type II, 130010
120260	Epiphyseal dysplasia, multiple, type 2, 600204
120435	Muir-Torre syndrome, 158320
120435	Colorectal cancer, hereditary, nonpolyposis, type 1 Ovarian cancer
120550	Clq deficiency, type A
120570	Clq deficiency, type B
120575	Clq deficiency, type C
120700	C3 deficiency
120950	C8 deficiency, type I
120960	C8 deficiency, type II
121050	Contractural arachnodactyly, congenital
121360	Myeloid leukemia, acute, M4Eo subtype
121800	Corneal dystrophy, crystalline, Schnyder
122720	Nicotine addiction, protection from
122720	Coumarin resistance, 122700
123000	Craniometaphyseal dysplasia
123270	[Creatine kinase, brain type, ectopic expression of]
123620	Cataract, cerulean, type 2, 601547
123660	Cataract, Coppock-like
123940	White sponge nevus, 193900
124030	Parkinsonism, susceptibility to
124030	Debrisoquine sensitivity
124200	Darier disease (keratosis follicularis)
125370	Dentatorubro-pallidoluysian atrophy
125660	Myopathy, desminopathic
125660	Cardiomyopathy
126090	Hyperphenylalaninemia due to pterin-4a-carbinolamine dehydratase
	1 - 1 por priori didiaminenta due to pierm - ta-caromoralime denyuratase

	deficiency, 264070
126337	Myxoid liposarcoma
126340	Xeroderma pigmentosum, group D, 278730
126391	DNA ligase I deficiency
126600	Drusen, radial, autosomal dominant
129010	Neuropathy, congenital hypomyelinating, 1
129900	EEC syndrome-1
130410	Glutaricaciduria, type IIB
130500	Elliptocytosis-1
131210	Atherosclerosis, susceptibility to
131244	Hirschsprung disease-2, 600155
131244	Eosinophilia, familial
132700	Cylindromatosis
133171	[Erythrocytosis, familial], 133100
133200	Erythrokeratodermia variabilis
133530	Xeroderma pigmentosum, group G, 278780
133701	Exostoses, multiple, type 2
133780	Vitreoretinopathy, exudative, familial
134790	
135300	Hyperferritinemia-cataract syndrome, 600886
135940	Fibromatosis, gingival
	Ichthyosis vulgaris, 146700
136132	[Fish-odor syndrome], 602079 Pfeiffer syndrome, 101600
136350	Ovarian dysgenesis, hypergonadotropic, with normal karyotype,
130433	233300
136550	Macular dystrophy, North Carolina type
136836	Fucosyltransferase-6 deficiency
138030	[Hyperproglucagonemia]
138040	Cortisol resistance
138140	Glucose transport defect, blood-brain barrier
138160	Diabetes mellitus, noninsulin-dependent
138160	Fanconi-Bickel syndrome, 227810
138300	Hemolytic anemia due to glutathione reductase deficiency
138570	Non-insulin dependent diabetes mellitus, susceptibility to
138700	[Apolipoprotein H deficiency]
138981	Pulmonary alveolar proteinosis, 265120
139250	Isolated growth hormone deficiency, Illig type with absent GH and
139230	Kowarski type with bioinactive GH
139350	Epidermolytic hyperkeratosis, 113800
139350	Keratoderma, palmoplantar, nonepidermolytic
140100	[Anhaptoglobinemia]
140100	[Hypohaptogloginemia]
141750	Alpha-thalassemia/mental retardation syndrome, type 1
141730	Methemoglobinemias, alpha-
141800	Thalassemias, alpha-
141800	Erythremias, alpha-
141800	Heinz body anemias, alpha-
141850	Themz body anemas, aipma- Thalassemia, alpha-
141850	Erythrocytosis
141850	Heinz body anemia
141850	Hemoglobin H disease
141850	<del> </del>
L14103U	Hypochromic microcytic anemia

142335	Hereditary persistence of fetal hemoglobin, heterocellular, Indian type
142600	Hemolytic anemia due to hexokinase deficiency
142989	Synpolydactyly, type II, 186000
143890	Hypercholesterolemia, familial
145001	Hyperparathyroidism-jaw tumor syndrome
145260	Pseudohypoaldosteronism, type II
145505	Hypertension, essential
145981	Hypocalciuric hypercalcemia, type II
146200	Hypoparathyroidism, familial
146760	[IgG receptor I, phagocytic, familial deficiency of]
146790	Lupus nephritis, susceptibility to
147141	Leukemia, acute lymphoblastic
147440	Growth retardation with deafness and mental retardation
147670	Rabson-Mendenhall syndrome
147670	Diabetes mellitus, insulin-resistant, with acanthosis nigricans
147670	Leprechaunism
147781	Atopy, susceptibility to
148040	Epidermolysis bullosa simplex, Koebner, Dowling-Meara, and
110010	Weber-Cockayne types, 131900, 131760, 131800
148041	Pachyonychia congenita, Jadassohn-Lewandowsky type, 167200
148043	Meesmann corneal dystrophy, 122100
148065	White sponge nevus, 193900
148070	Liver disease, susceptibility to, from hepatotoxins or viruses
148080	Epidermolytic hyperkeratosis, 113800
148370	Keratolytic winter erythema
148900	Klippel-Feil syndrome with laryngeal malformation
150200	[Placental lactogen deficiency]
150210	Lactoferrin-deficient neutrophils, 245480
150292	Epidermolysis bullosa, Herlitz junctional type, 226700
151440	Leukemia, T-cell acute lymphoblastoid
151670	Hepatic lipase deficiency
152427	Long QT syndrome-2
152445	Vohwinkel syndrome, 124500
152445	Erythrokeratoderma, progressive symmetric, 602036
152760	Hypogonadotropic hypogonadism due to GNRH deficiency, 227200
152780	Hypogonadism, hypergonadotropic
152780	Male pseudohermaphroditism due to defective LH
152790	Precocious puberty, male, 176410
152790	Leydig cell hypoplasia
153454	Ehlers-Danlos syndrome, type VI, 225400
153455	Cutis laxa, recessive, type I, 219100
154275	Malignant hyperthermia susceptibility 2
154276	Malignant hyperthermia susceptibility 3
154545	Chronic infections, due to opsonin defect
154550	Carbohydrate-deficient glycoprotein syndrome, type Ib, 602579
155555	[Red hair/fair skin]
155555	UV-induced skin damage, vulnerability to
156232	Mesomelic dysplasia, Kantaputra type
156850	Cataract, congenital, with microphthalmia
157147	Abetalipoproteinemia, 200100

157170	Holoprosencephaly-2
157640	PEO with mitochondrial DNA deletions, type 1
158590	Spinal muscular atrophy-4
159000	Muscular dystrophy, limb-girdle, type 1A
159001	Muscular dystrophy, limb-girdle, type 1B
160760	Cardiomyopathy, familial hypertrophic, 1, 192600
160760	Central core disease, one form
160781	Cardiomyopathy, hypertrophic, mid-left ventricular chamber type
160900	Myotonic dystrophy
162150	Obestiy with impaired prohormone processing, 600955
162200	Neurofibromatosis, type 1
162200	Watson syndrome, 193520
162400	Neuropathy, hereditary sensory and autonomic, type 1
163729	Hypertension, pregnancy-induced
163950	Noonan syndrome-1
163950	Cardiofaciocutaneous syndrome, 115150
164731	Ovarian carcinoma, 167000
164770	Myeloid malignancy, predisposition to
164953	Liposarcoma
167410	Rhabdomyosarcoma, alveolar, 268220
168360	Paraneoplastic sensory neuropathy
168450	Hypoparathyroidism, autosomal dominant
168450	Hypoparathyroidism, autosomal recessive
168468	Metaphyseal chondrodysplasia, Murk Jansen type, 156400
168500	Parietal foramina
169600	Hailey-Hailey disease
170500	Myotonia congenita, atypical acetazolamide-responsive
170500	Paramyotonia congenita, 168300
170500	Hyperkalemic periodic paralysis
171190	Hypertension, essential, 145500
171190	Lysosomal acid phosphatase deficiency
171760	Hypophosphatasia, adult, 146300
171760	Hypophosphatasia, adult, 140500  Hypophosphatasia, infantile, 241500
172400	Hemolytic anemia due to glucosephosphate isomerase deficiency
172400	Hydrops fetalis, one form
172430	Enolase deficiency
172471	Glycogenosis, hepatic, autosomal
172471	Phosphorylase kinase deficiency of liver and muscle, 261750
173470	Glanzmann thrombasthenia, type B
173610	Platelet alpha/delta storage pool deficiency
173850	Polio, susceptibility to
173870	Xeroderma pigmentosum
173870	Fanconi anemia
173910	Polycystic kidney disease, adult, type II
174000	Medullary cystic kidney disease, AD
174900	Polyposis, juvenile intestinal
176100	Porphyria cutanea tarda
176100	<del></del>
176450	Porphyria, hepatoerythropoietic
176830	Sacral agenesis-1 Obesity, adrenal insufficiency, and red hair
176830 176930	Dysprothrombinemia
1 / 137 311	į Dyspiounomonicinia

176030	Hypoprothrombinemia
176930	Pituitary tumor, invasive
176960	Apnea, postanesthetic
177400	
178300	Ptosis, hereditary congenital, 1 Pulmonary hypertension, familial primary
178600	
178640	Pulmonary alveolar proteinosis, congenital, 265120
179095	Male infertility
179755	Renal cell carcinoma, papillary, 1
180069	Retinal dystrophy, autosomal recessive, childhood-onset
180069	Retinitis pigmentosa-20
180069	Leber congenital amaurosis-2, 204100
180071	Retinitis pigmentosa, autosomal recessive
180100	Retinitis pigmentosa-1
180105	Retinitis pigmentosa-10
180380	Night blindness, congenital stationery, rhodopsin-related
180380	Retinitis pigmentosa, autosomal recessive
180380	Retinitis pigmentosa-4, autosomal dominant
180901	Malignant hyperthermia susceptibility 1, 145600
180901	Central core disease, 117000
181405	Scapuloperoneal spinal muscular atrophy, New England type
181430	Scapuloperoneal syndrome, myopathic type
181460	Schistosoma mansoni, susceptibility/resistance to
182138	Anxiety-related personality traits
182280	Small-cell cancer of lung
182290	Smith-Magenis syndrome
182380	Glucose/galactose malabsorption
182381	Renal glucosuria, 253100
182600	Spastic paraplegia-3A
182601	Spastic paraplegia-4
182860	Pyropoikilocytosis
182860	Spherocytosis, recessive
182860	Elliptocytosis-2
182900	Spherocytosis-2
185800	Symphalangism, proximal
186580	Arthrocutaneouveal granulomatosis
186880	Leukemia/lymphoma, T-cell
186921	Leukemia, T-cell acute lymphoblastic
187040	Leukemia-1, T-cell acute lymphoblastic
188070	Bleeding disorder due to defective thromboxane A2 receptor
188450	Goiter, adolescent multinodular
188450	Goiter, nonendemic, simple
188450	Hypothyroidism, hereditary congenital
188826	Sorsby fundus dystrophy, 136900
189800	Preeclampsia/eclampsia
190040	Meningioma, SIS-related
190040	Dermatofibrosarcoma protuberans
190040	Giant-cell fibroblastoma
190195	Ichthyosiform erythroderma, congenital, 242100
190195	Ichthyosis, lamellar, autosomal recessive, 242300
190198	Leukemia, T-cell acute lymphoblastic
190300	Tremor, familial essential, 1
190605	Triphalangeal thumb-polysyndactyly syndrome

191044	Cardiomyopathy, familial hypertrophic
191092	Tuberous sclerosis-2
191315	Insensitivity to pain, congenital, with anhidrosis, 256800
192090	Ovarian carcinoma
192090	Breast cancer, lobular
192090	Endometrial carcinoma
192090	Gastric cancer, familial, 137215
192340	Diabetes insipidus, neurohypophyseal, 125700
192974	Neonatal alloimmune thrombocytopenia
192974	Glycoprotein Ia deficiency
193300	Renal cell carcinoma
193300	von Hippel-Lindau syndrome
193500	Rhabdomyosarcoma, alveolar, 268220
193500	Waardenburg syndrome, type I
193500	Waardenburg syndrome, type III, 148820
J	
193500	Craniofacial-deafness-hand syndrome, 122880  Acyl-CoA dehydrogenase, medium chain, deficiency of
201450	
201460	Acyl-CoA dehydrogenase, long chain, deficiency of
201475	VLCAD deficiency
201810	3-beta-hydroxysteroid dehydrogenase, type II, deficiency
203300	Hermansky-Pudlak syndrome
203500	Alkaptonuria
205100	Amyotrophic lateral sclerosis, juvenile
205900	Anemia, Diamond-Blackfan
207750	Hyperlipoproteinemia, type Ib
208250	Jacobs syndrome
208400	Aspartylglucosaminuria
212138	Carnitine-acylcarnitine translocase deficiency
216550	Cohen syndrome
216900	Achromatopsia
217300	Cornea plana congenita, recessive
217800	Macular corneal dystrophy
218030	Apparent mineralocorticoid excess, hypertension due to
221770	Polycystic lipomembranous osteodysplasia with sclerosing
L	leukencephalopathy
221820	Gliosis, familial progressive subcortical
222700	Lysinuric protein intolerance
222745	DECR deficiency
222800	Hemolytic anemia due to bisphosphoglycerate mutase deficiency
222900	Sucrose intolerance
225500	Ellis-van Creveld syndrome
227645	Fanconi anemia, type C
227646	Fanconi anemia, type D
227650	Fanconi anemia, type A
229700	Fructose-bisphosphatase deficiency
229800	[Fructosuria]
230000	Fucosidosis
230400	Galactosemia
230800	Gaucher disease
230800	Gaucher disease with cardiovascular calcification
231550	Achalasia-addisonianism-alacrimia syndrome
231670	Glutaricaciduria, type I

231675	Glutaricaciduria, type IIC
231680	Glutaricaciduria, type IIC
232300	Glycogen storage disease II
232700	Glycogen storage disease VI
232800	Glycogen storage disease VII
233700	Chronic granulomatous disease due to deficiency of NCF-1
234200	Neurodegeneration with brain iron accumulation
236250	Homocystinuria due to MTHFR deficiency
236730	Urofacial syndrome
237300	Carbamoylphosphate synthetase I deficiency
239100	Van Buchem disease
240400	Scurvy
245200	Krabbe disease
245900	Norum disease
245900	Fish-eye disease
246450	HMG-CoA lyase deficiency
248510	Mannosidosis, beta-
248600	Maple syrup urine disease, type Ia
248610	Maple syrup urine disease, type II
249000	Meckel syndrome
250250	Cartilage-hair hypoplasia
250790	Methemoglobinemia due to cytochrome b5 deficiency
250850	Hypermethioninemia, persistent, autosomal dominant, due to
	methionine adenosyltransferase I/III deficiency
251170	Mevalonicaciduria
251600	Microphthalmia, autosomal recessive
252500	Mucolipidosis II
252500	Mucolipidosis III
252900	Sanfilippo syndrome, type A
253000	Mucopolysaccharidosis IVA
253250	Mulibrey nanism
255800	Schwartz-Jampel syndrome
256030	Nemaline myopathy-2
256540	Galactosialidosis
256700	Neuroblastoma
256731	Ceroid-lipofuscinosis, neuronal-5, variant late infantile
257200	Niemann-Pick disease, type A
257200	Niemann-Pick disease, type B
258501	3-methylglutaconicaciduria, type III
258900	Oroticaciduria
259900	Hyperoxaluria, primary, type 1
262000	Bjornstad syndrome
266200	Anemia, hemolytic, due to PK deficiency
270100	Situs inversus viscerum
270200	Sjogren-Larsson syndrome
272750	GM2-gangliosidosis, AB variant
272800	Tay-Sachs disease
272800	[Hex A pseudodeficiency]
272800	GM2-gangliosidosis, juvenile, adult
273800	Thrombocytopenia, neonatal alloimmune
273800	Glanzmann thrombasthenia, type A
276600	Tyrosinemia, type II

276700	Tyrosinemia, type I
276710	Tyrosinemia, type III
276900	Usher syndrome, type 1A
276901	Usher syndrome, type 2
276902	Usher syndrome, type 3
277700	Werner syndrome
278700	Xeroderma pigmentosum, group A
278760	Xeroderma pigmentosum, group F
300000	Opitz G syndrome, type I
300008	Nephrolithiasis, type I, 310468
300008	Proteinuria, low molecular weight, with hypercalciuric
300000	nephrocalcinosis
300008	Dent disease, 300009
300008	Hypophosphatemia, type III
300011	Menkes disease, 309400
300011	Occipital horn syndrome, 304150
300011	Cutis laxa, neonatal
300031	Mental retardation, X-linked, FRAXF type
300044	Wernicke-Korsakoff syndrome, susceptibility to
300044	Mental retardation, X-linked 23, nonspecific
300047	Mental retardation, X-linked 20
300048	Intestinal pseudoobstruction, neuronal, X-linked
300049	Nodular heterotopia, bilateral periventricular
300049	BPNH/MR syndrome
300055	Mental retardation with psychosis, pyramidal signs, and
300000	macroorchidism
300066	Deafness, X-linked 6, sensorineural
300071	Night blindness, congenital stationary, type 2
300075	Coffin-Lowry syndrome, 303600
300077	Mental retardation, X-linked 29
300100	Adrenoleukodystrophy
300100	Adrenomyeloneuropathy
300104	Mental retardation, X-linked nonspecific, 309541
300110	Night blindness, congenital stationary, X-linked incomplete,
	300071
300123	Mental retardation with isolated growth hormone deficiency
300126	Dyskeratosis congenita-1, 305000
300127	Mental retardation, X-linked, 60
300310	Agammaglobulinemia, type 2, X-linked
300600	Ocular albinism, Forsius-Eriksson type
301000	Thrombocytopenia, X-linked, 313900
301000	Wiskott-Aldrich syndrome
301200	Amelogenesis imperfecta
301201	Amelogenesis imperfecta-3, hypoplastic type
301220	Partington syndrome II
301590	Anophthalmos-1
301830	Arthrogryposis, X-linked (spinal muscular atrophy, infantile, X-
	linked)
301835	Arts syndrome
301845	Bazex syndrome
302060	Noncompaction of left ventricular myocardium, isolated
302060	Barth syndrome

302060	Cardiomyopathy, X-linked dilated, 300069
302060	Endocardial fibroelastosis-2
302350	Nance-Horan syndrome
	Charcot-Marie-Tooth neuropathy, X-linked-2, recessive
302801	Chondrodysplasia punctata, X-linked dominant
302960	Colorblindness, blue monochromatic
303700	
303800	Colorblindness, deutan
303900	Colorblindness, protan
304040	Charcot-Marie-Tooth neuropathy, X-linked-1, dominant, 302800
304050	Aicardi syndrome
304110	Craniofrontonasal dysplasia
304800	Diabetes insipidus, nephrogenic
305100	Anhidrotic ectodermal dysplasia
305435	Heterocellular hereditary persistence of fetal hemoglobin, Swiss
 	type
305450	FG syndrome
305900	Favism
305900	G6PD deficiency
305900	Hemolytic anemia due to G6PD deficiency
306000	Glycogenosis, X-linked hepatic, type I
306000	Glycogenosis, X-linked hepatic, type II
306100	Gonadal dysgenesis, XY female type
306700	Hemophilia A
306995	[Homosexuality, male]
307150	Hypertrichosis, congenital generalized
307800	Hypophosphatemia, hereditary
308310	Incontinentia pigmenti, familial
308800	Keratosis follicularis spinulosa decalvans
308840	Spastic paraplegia, 312900
308840	Hydrocephalus due to aqueductal stenosis, 307000
308840	MASA syndrome, 303350
309200	Manic-depressive illness, X-linked
309470	Mental retardation, X-linked, syndromic-3, with spastic diplegia
309500	Renpenning syndrome-1
309510	Mental retardation, X-linked, syndromic-1, with dystonic
	movements, ataxia, and seizures
309530	Mental retardation, X-linked 1, non-dysmorphic
309548	Mental retardation, X-linked, FRAXE type
309585	Mental retardation, X-linked, syndromic-6, with gynecomastia and
	obesity
309605	Mental retardation, X-linked, syndromic-4, with congenital
	contractures and low fingertip arches
309610	Mental retardation, X-linked, syndromic-2, with dysmorphism and
	cerebral atrophy
309620	Mental retardation-skeletal dysplasia
309850	Brunner syndrome
309900	Mucopolysaccharidosis II
310300	Emery-Dreifuss muscular dystrophy
310400	Myotubular myopathy, X-linked
310460	Myopia-1
310460	Bornholm eye disease
310490	Cowchock syndrome

211050	Ontic strength V limited
311050	Optic atrophy, X-linked
311200	Oral-facial-digital syndrome 1
311300	Otopalatodigital syndrome, type I
311510	Waisman parkinsonism-mental retardation syndrome
311850	Phosphoribosyl pyrophosphate synthetase-related gout
312040	N syndrome, 310465
312060	Properdin deficiency, X-linked
312170	Pyruvate dehydrogenase deficiency
312700	Retinoschisis
312760	Turner syndrome
313400	Spondyloepiphyseal dysplasia tarda
313700	Perineal hypospadias
313700	Prostate cancer
313700	Spinal and bulbar muscular atrophy of Kennedy, 313200
313700	Breast cancer, male, with Reifenstein syndrome
313700	Androgen insensitivity, several forms
314250	Dystonia-3, torsion, with parkinsonism, Filipino type
314300	Goeminne TKCR syndrome
314400	Cardiac valvular dysplasia-1
314580	Wieacker-Wolff syndrome
600040	Colorectal cancer
600079	Colon cancer
600101	Deafness, autosomal dominant 2
600119	Muscular dystrophy, Duchenne-like, type 2
600119	Adhalinopathy, primary
600138	Retinitis pigmentosa-11
600140	Rubenstein-Taybi syndrome, 180849
600163	Long QT syndrome-3
600173	SCID, autosomal recessive, T-negative/B-positive type
600175	Spinal muscular atrophy, congenital nonprogressive, of lower limbs
600194	Ichthyosis bullosa of Siemens, 146800
600223	Spinocerebellar ataxia-4
600231	Palmoplantar keratoderma, Bothnia type
600234	HMG-CoA synthease-2 deficiency
600243	Temperature-sensitive apoptosis
600258	Colorectal cancer, hereditary nonpolyposis, type 3
600266	Resistance/susceptibility to TB, etc.
600273	Polycystic kidney disease, infantile severe, with tuberous sclerosis
600276	Cerebral arteriopathy with subcortical infarcts and
Ĺ	leukoencephalopathy, 125310
600281	Non-insulin-dependent diabetes mellitus, 125853
600281	MODY, type 1, 125850
600309	Atrioventricular canal defect-1
600310	Pseudoachondroplasia, 177170
600310	Epiphyseal dysplasia, multiple 1, 132400
600320	Insulin-dependent diabetes mellitus-5
600332	Rippling muscle disease-1
600359	Bartter syndrome, type 2
600374	Bardet-Biedl syndrome 4
600510	Pigment dispersion syndrome
600512	Epilepsy, partial
600525	Trichodontoosseous syndrome, 190320
600525	Trichodontoosseous syndrome, 190320

600536	Myopathy, congenital
600593	Craniosynostosis, Adelaide type
	Lipoid adrenal hyperplasia, 201710
600617	<u></u>
600623	Prostate cancer, 176807
600631	Enuresis, nocturnal, 1
600650	Myopathy due to CPT II deficiency, 255110
600650	CPT deficiency, hepatic, type II, 600649
600652	Deafness, autosomal dominant 4
600698	Salivary adenoma
600698	Uterine leiomyoma
600698	Lipoma
600698	Lipomatosis, mutiple, 151900
600722	Ceroid lipofuscinosis, neuronal, variant juvenile type, with granular
	osmiophilic deposits
600722	Ceroid lipofuscinosis, neuronal-1, infantile, 256730
600725	Holoprosencephaly-3, 142945
600757	Orofacial cleft-3
600759	Alzheimer disease-4
600792	Deafness, autosomal recessive 5
600807	Bronchial asthma
600808	Enuresis, nocturnal, 2
600811	Xeroderma pigmentosum, group E, DDB-negative subtype, 278740
600850	Schizophrenia disorder-4
600852	Retinitis pigmentosa-17
600881	Cataract, congenital, zonular, with sutural opacities
600882	Charcot-Marie-Tooth neuropathy-2B
600897	Cataract, zonular pulverulent-1, 116200
600918	Cystinuria, type III
600956	Persistent Mullerian duct syndrome, type II, 261550
600957	Persistent Mullerian duct syndrome, type I, 261550
600958	Cardiomyopathy, familial hypertrophic, 4, 115197
600968	Gitelman syndrome, 263800
600975	Glaucoma 3, primary infantile, B
600995	Nephrotic syndrome, idiopathic, steroid-resistant
600996	Arrhythmogenic right ventricular dysplasia-2
601097	Neuropathy, recurrent, with pressure palsies, 162500
601097	Charcot-Marie-Tooth neuropathy-1A, 118220
601097	Dejerine-Sottas disease, PMP22 related, 145900
601105	Pycnodysostosis, 265800
601199	Neonatal hyperparathyroidism, 239200
601199	Hypocalcemia, autosomal dominant, 601198
601199	Hypocalciuric hypercalcemia, type I, 145980
601238	Cerebellar ataxia, Cayman type
601277	Ichthyosis, lamellar, type 2
601284	Hereditary hemorrhagic telangiectasia-2, 600376
601295	Bile acid malabsorption, primary
601309	Basal cell carcinoma, sporadic
601309	Basal cell nevus syndrome, 109400
	Polycystic kidney disease, adult type I, 173900
601313	Deafness, autosomal dominant 9
601369	+
601386	Deafness, autosomal recessive 12
601402	Leukemia, myeloid, acute

(01412	Desfraça outocomol dominant 7
601412	Deafness, autosomal dominant 7
601414	Retinitis pigmentosa-18
601458	Inflammatory bowel disease-2
601493	Cardiomyopathy, dilated 1C
601517	Spinocerebellar ataxia-2, 183090
601518	Prostate cancer, hereditary, 1, 176807
601596	Charcot-Marie-Tooth neuropathy, demyelinating
601604	Mycobacterial and salmonella infections, susceptibility to
601650	Paraganglioma, familial nonchromaffin, 2
601652	Glaucoma 1A, primary open angle, juvenile-onset, 137750
601669	Hirschsprung disease, one form
601676	Acute insulin response
601682	Glaucoma 1C, primary open angle
601691	Retinitis pigmentosa-19, 601718
601691	Stargardt disease-1, 248200
601691	Cone-rod dystrophy 3
601691	Fundus flavimaculatus with macular dystrophy, 248200
601692	Reis-Bucklers corneal dystrophy
601692	Corneal dystrophy, Avellino type
601692	Corneal dystrophy, Groenouw type I, 121900
601692	Corneal dystrophy, lattice type I, 122200
601718	Retinitis pigmentosa-19
601744	Systemic lupus erythematosus, susceptibility to, 1
601769	Osteoporosis, involutional
601769	Rickets, vitamin D-resistant, 277440
601771	Glaucoma 3A, primary infantile, 231300
601780	Ceroid-lipofuscinosis, neuronal-6, variant late infantile
601785	Carbohydrate-deficient glycoprotein syndrome, type I, 212065
601843	Hypothyroidism, congenital, 274400
601844	Pseudohypoaldosteronism type II
601846	Muscular dystrophy with rimmed vacuoles
601863	Bare lymphocyte syndrome, complementation group C
601928	Monilethrix, 158000
601954	Muscular dystrophy, limb-girdle, type 2G
601975	Ectodermal dysplasia/skin fragility syndrome
602025	Obesity/hyperinsulinism, susceptibility to
602078	Fibrosis of extraocular muscles, congenital, 2
602085	Postaxial polydactyly, type A2
602086	Arrhythmogenic right ventricular dysplasia-3
602088	Nephronophthisis, infantile
602089	Hemangioma, capillary, hereditary
602092	Deafness, autosomal recessive 18
602094	Lipodystrophy, familial partial
602116	Glioma
602121	Deafness, autosomal dominant nonsyndromic sensorineural, 1,
	124900
602134	Tremor, familial essential, 2
602136	Refsum disease, infantile, 266510
602136	Zellweger syndrome-1, 214100
602136	Adrenoleukodystrophy, neonatal, 202370
602153	Monilethrix, 158000
602216	Peutz-Jeghers syndrome, 175200
002210	1 Tues deBrief Syndrome, 170200

602225	Cone-rod retinal dystrophy-2, 120970
602225	Leber congenital amaurosis, type III
602279	Oculopharyngeal muscular dystorphy, 164300
602279	Oculopharyngeal muscular dystrophy, autosomal recessive, 257950
602363	Ellis-van Creveld-like syndrome
602403	Alzheimer disease, susceptibility to
602447	Coronary artery disease, susceptibility to
602460	Deafness, autosomal dominant 15, 602459
602477	Febrile convulsions, familial, 2
602491	Hyperlipidemia, familial combined, 1
602522	Bartter syndrome, infantile, with sensorineural deafness
602568	Homocystinuria-megaloblastic anemia, cbl E type, 236270
602574	Deafness, autosomal dominant 12, 601842
602574	Deafness, autosomal dominant 8, 601543
602629	Dystonia-6, torsion
602666	Deafness, autosomal recessive 3, 600316
602716	Nephrosis-1, congenital, Finnish type, 256300
602772	Retinitis pitmentosa-24
602782	Faisalabad histiocytosis
602783	Spastic paraplegia-7

## Mature Polypeptides

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The present invention also encompasses mature forms of a polypeptide having the amino acid sequence of SEQ ID NO:Y and/or the amino acid sequence encoded by the cDNA in a deposited clone. Polynucleotides encoding the mature forms (such as, for example, the polynucleotide sequence in SEO ID NO:X and/or the polynucleotide sequence contained in the cDNA of a deposited clone) are also encompassed by the invention. Moreover, fragments or variants of these polypeptides (such as, fragments as described herein, polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to these polypeptides, or polypeptides encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of the polynucleotide encoding these polypeptides) are also encompassed by the invention. In preferred embodiments, these fragments or variants retain one or more functional acitivities of the full-length or mature form of the polypeptide (e.g., biological activity (such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative disorders), antigenicity (ability to bind, or compete with a polypeptide of the invention for binding, to an anti-polypeptide of the invention antibody), immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention). Antibodies that bind the polypeptides of the invention, and polynucleotides encoding these polypeptides are also encompassed by the invention.

According to the signal hypothesis, proteins secreted by mammalian cells have a signal or secretary leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Most mammalian cells and even insect cells cleave secreted proteins with the same specificity. However, in some cases, cleavage of a secreted protein is not entirely uniform, which results in two or more mature species of the protein. Further, it has long been known that cleavage specificity of a secreted protein is ultimately determined by the primary structure of the complete protein, that is, it is inherent in the amino acid sequence of the polypeptide.

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1A.

In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, the predicted mature form of the polypeptide as delineated in columns 14 and 15 of Table 1A. Moreover, fragments or variants of these polypeptides (such as, fragments as described herein, polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to these polypeptides, or polypeptides encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of the polynucleotide encoding these polypeptides) are also encompassed by the invention. In preferred embodiments, these fragments or variants retain one or more functional acitivities of the full-length or mature form of the polypeptide (e.g., biological activity (such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative disorders), antigenicity (ability to bind, or compete with a polypeptide of the invention for binding, to an antipolypeptide of the invention antibody), immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention).

Antibodies that bind the polypeptides of the invention, and polynucleotides encoding these polypeptides are also encompassed by the invention.

Polynucleotides encoding proteins comprising, or consisting of, the predicted mature form of polypeptides of the invention (e.g., polynucleotides having the sequence of SEQ ID NO: X (Table 1A, column 4), the sequence delineated in columns 7 and 8 of Table 1A, and a sequence encoding the mature polypeptide delineated in columns 14 and 15 of Table 1A (e.g., the sequence of SEQ ID NO:X encoding the mature polypeptide delineated in columns 14 and 15 of Table 1)) are also encompassed by the invention, as are fragments or variants of these polynucleotides (such as, fragments as described herein, polynucleotides at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to these polyncueotides, and nucleic acids which hybridizes under stringent conditions to the complementary strand of the polynucleotide).

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 15 residues of the predicted cleavage point (i.e., having 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 more or less contiguous residues of SEQ ID NO:Y at the N-terminus when compared to the predicted mature form of the polypeptide (e.g., the mature polypeptide delineated in columns 14 and 15 of Table 1). Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. Nonetheless, the present invention provides the mature protein produced by expression of the polynucleotide sequence of SEQ ID NO:X and/or the polynucleotide sequence contained in the cDNA of a deposited clone, in a mammalian cell (e.g., COS cells, as desribed below). These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

## Polynucleotide and Polypeptide Variants

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The present invention is also directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, nucleotide sequences encoding the polypeptide of SEQ ID NO:Y, the nucleotide sequence of SEQ ID NO:X that encodes the polypeptide sequence as defined in columns 13 and 14 of Table 1A, nucleotide sequences encoding the polypeptide sequence as defined in columns 13 and 14 of Table 1A, the nucleotide

sequence of SEQ ID NO:X encoding the polypeptide sequence as defined in Table 1B, the nucleotide sequence as defined in columns 8 and 9 of Table 2, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, the nucleotide sequence as defined in column 6 of Table 1C, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in column 6 of Table 1C, the cDNA sequence contained in ATCC Deposit No:Z, nucleotide sequences encoding the polypeptide encoded by the cDNA sequence contained in ATCC Deposit No:Z, and/or nucleotide sequences encoding a mature (secreted) polypeptide encoded by the cDNA sequence contained in ATCC Deposit No:Z.

The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y, the polypeptide as defined in columns 13 and 14 of Table 1A, the polypeptide sequence as defined in columns 6 and 7 of Table 1B.1, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, a polypeptide sequence encoded by the nucleotide sequence as defined in column 6 of Table 1C, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, the polypeptide sequence encoded by the cDNA sequence contained in ATCC Deposit No:Z and/or a mature (secreted) polypeptide encoded by the cDNA sequence contained in ATCC Deposit No:Z.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence described in SEQ ID NO:X or contained in the cDNA sequence of ATCC Deposit No:Z; (b) a nucleotide sequence in SEQ ID NO:X or the cDNA in ATCC Deposit No:Z which encodes the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; (c) a nucleotide sequence in SEQ ID NO:X or the cDNA in ATCC Deposit No:Z which encodes a mature polypeptide (i.e., a secreted polypeptide (e.g., as delineated in columns 14 and 15 of Table 1A)); (d) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of ATCC Deposit No:Z, which encodes a biologically active fragment of a polypeptide; (e) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of ATCC Deposit No:Z, which encodes an antigenic fragment of a polypeptide; (f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; (g) a nucleotide sequence encoding a mature polypeptide of the amino acid sequence of SEQ ID NO:Y (i.e., a secreted polypeptide (e.g., as delineated in columns 14 and 15

of Table 1A)) or a mature polypeptide of the amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; (h) a nucleotide sequence encoding a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; (i) a nucleotide sequence encoding an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; and (j) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), or (i) above.

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The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j) above, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the cDNA contained in ATCC Deposit No:Z or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, the nucleotide coding sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, the nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1C or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1C or the complementary strand thereto, the nucleotide sequence in SEQ ID NO:X encoding the polypeptide sequence as defined in columns 6 and 7 of Table 1B.1 or the complementary strand thereto, nucleotide sequences encoding the polypeptide as defined in column 6 and 7 of Table 1B.1 or the complementary strand thereto, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides and nucleic acids.

In a preferred embodiment, the invention encompasses nucleic acid molecules which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), (h), or (i), above, as are polypeptides encoded by these polynucleotides. In another preferred embodiment, polynucleotides which hybridize to the

complement of these nucleic acid molecules under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

In another embodiment, the invention provides a purified protein comprising, or alternatively consisting of, a polypeptide having an amino acid sequence selected from the group consisting of: (a) the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; (b) the amino acid sequence of a mature (secreted) form of a polypeptide having the amino acid sequence of SEQ ID NO:Y (e.g., as delineated in columns 14 and 15 of Table 1A) or a mature form of the amino acid sequence encoded by the cDNA in ATCC Deposit No:Z mature; (c) the amino acid sequence of a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z; and (d) the amino acid sequence of an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in ATCC Deposit No:Z.

The present invention is also directed to proteins which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the amino acid sequences in (a), (b), (c), or (d), above, the amino acid sequence shown in SEQ ID NO:Y, the amino acid sequence encoded by the cDNA contained in ATCC Deposit No:Z, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1C, the amino acid sequence as defined in columns 6 and 7 of Table 1B.1, an amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X, and an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X. Fragments of these polypeptides are also provided (e.g., those fragments described herein). Further proteins encoded by polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these amino acid sequences under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are the polynucleotides encoding these proteins.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to

5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referred to in Table 1B or 2 as the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that

there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

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By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence of a polypeptide referred to in Table 1A (e.g., the amino acid sequence delineated in columns 14 and 15) or a fragment thereof, Table 1B.1 (e.g., the amino acid sequence identified in column 6) or a fragment thereof, Table 2 (e.g., the amino acid sequence of the polypeptide encoded by the polynucleotide sequence defined in columns 8 and 9 of Table 2) or a fragment thereof, the amino acid sequence of the polypeptide encoded by the polynucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1C or a fragment thereof, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence of the polypeptide encoded by cDNA contained in ATCC Deposit No:Z, or a fragment thereof, the amino acid sequence of a mature (secreted) polypeptide encoded by cDNA contained in ATCC Deposit No:Z, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237-245 (1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence,

whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The polynucleotide variants of the invention may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, polypeptide variants in which less than 50, less than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also

preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

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Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. As an example, Ron et al. (J. Biol. Chem. 268: 2984-2988 (1993)) reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem. 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a biological or functional activity of the polypeptides of the invention (such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cardiovascular disorders). Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, (e.g., encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); (3) Northern Blot analysis for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues); and (4) in situ hybridization (e.g., histochemistry) for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues).

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having functional activity. By a polypeptide having "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein and/or a mature (secreted) protein of the invention. Such functional activities include, but are not limited to, biological activity (such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative diseases and disorders), antigenicity (ability to bind, or compete with a polypeptide of the invention for binding, to an anti-polypeptide of the invention antibody), immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention.

The functional activity of the polypeptides, and fragments, variants and derivatives of the invention, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with a full-length polypeptide of the present invention for binding to an anti-polypetide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel

diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, the ability of physiological correlates of a polypeptide of the present invention to bind to a substrate(s) of the polypeptide of the invention can be routinely assayed using techniques known in the art.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants and derivatives thereof to elicit polypeptide related biological activity (either *in vitro* or *in vivo*). Other methods will be known to the skilled artisan and are within the scope of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA contained in ATCC Deposit No:Z, the nucleic acid sequence referred to in Table 1B (SEQ ID NO:X), the nucleic acid sequence disclosed in Table 1A (e.g., the nucleic acid sequence delineated in columns 7 and 8), the nucleic acid sequence disclosed in Table 2 (e.g., the nucleic acid sequence delineated in columns 8 and 9) or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. See Cunningham and Wells, Science 244:1081-1085 (1989). The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitutions with one or more of the amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, serum albumin (preferably human serum albumin) or a fragment thereof, or leader or secretory sequence, or a sequence facilitating purification, or (v) fusion of the polypeptide with another compound, such as albumin (including but not limited to recombinant albumin (see, e.g., U.S. Patent No. 5,876,969,

issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. See Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).

A further embodiment of the invention relates to polypeptides which comprise the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions from a polypeptide sequence disclosed herein. Of course it is highly preferable for a polypeptide to have an amino acid sequence which, for example, comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, the amino acid sequence of the mature (e.g., secreted) polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columnns 8 and 9 of Table 2, an amino acid sequence encoded by the complement of SEQ ID NO:X, an amino acid sequence encoded by cDNA contained in ATCC Deposit No:Z, and/or the amino acid sequence of a mature (secreted) polypeptide encoded by cDNA contained in ATCC Deposit No:Z, or a fragment thereof, which contains, in order of everincreasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions.

In specific embodiments, the polypeptides of the invention comprise, or alternatively, consist of, fragments or variants of a reference amino acid sequence selected from: (a) the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature formand/or other fragments described herein); (b) the amino acid sequence encoded by SEQ ID NO:X or fragments thereof; (c) the amino acid sequence encoded by the complement of SEQ ID NO:X or fragments thereof; (d) the amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or fragments thereof; and (e) the amino acid sequence encoded by cDNA contained in ATCC Deposit No:Z or fragments thereof; wherein the fragments or variants have 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, amino acid residue additions, substitutions, and/or deletions when compared to the reference amino acid sequence. In preferred embodiments, the amino acid substitutions are conservative. Polynucleotides encoding these polypeptides are also encompassed by the invention.

# Polynucleotide and Polypeptide Fragments

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The present invention is also directed to polynucleotide fragments of the polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers to a polynucleotide having a nucleic acid sequence which, for example: is a portion of the cDNA contained in ATCC Deposit No:Z or the complementary strand thereto; is a portion of the polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in ATCC Deposit No:Z or the complementary strand thereto; is a portion of the polynucleotide sequence encoding the mature (secreted) polypeptide encoded by the cDNA contained in ATCC Deposit No:Z or the complementary strand thereto; is a portion of a polynucleotide sequence encoding the mature amino acid sequence as defined in columns 14 and 15 of Table 1A or the complementary strand thereto; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is a portion of the polynucleotide sequence of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is a portion of the polynucleotide sequence in SEQ ID NO:X or the complementary strand thereto; is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X; is a polynucleotide sequence encoding a portion of a polypeptide encoded by the complement of the polynucleotide sequence in SEQ ID NO:X; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:B as defined in column 6 of Table 1C or the complementary strand thereto; or is a portion of the polynucleotide sequence of SEQ ID NO:B as defined in column 6 of Table 1C or the complementary strand thereto.

The polynucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in ATCC Deposit No:Z, or the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 160, 170, 180, 190, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

Moreover, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-

1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-5 3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-10 5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-15 7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity; such as, for example, activity useful in detecting, preventing, diagnosing, 20 prognosticating, treating, and/or ameliorating cancer and other hyperproliferative diseases and disorders). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides. 25

Further representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-

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4350, 4351-4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of the cDNA sequence contained in ATCC Deposit No:Z, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

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Moreover, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence delineated in Table 1C column 6. Additional, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence that is the complementary strand of a sequence delineated in column 6 of Table 1C. In further embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1C, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1C, column 5). In additional embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1C, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated Table 1C, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1C, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by

the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1C, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1C, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

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In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1C which correspond to the same ATCC Deposit No:Z (see Table 1C, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A, 1B, or 1C) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in the same row of column 6 of Table 1C, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A, 1B, or 1C) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X (e.g., as described herein) are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also

encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1C are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1C is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1C, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of the amino acid sequence contained in SEQ ID NO:Y, is a portion of the mature form of SEQ ID NO:Y as defined in columns 14 and 15 of Table 1A, a portion of an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, is a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, is a portion of an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, is a portion of the amino acid sequence of a mature (secreted) polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or is a portion of an amino acid sequence

encoded by the cDNA contained in ATCC Deposit No:Z. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of cDNA and SEQ ID NO: Y. In a preferred embodiment, polypeptide fragments of the invention include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

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Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities; such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative diseases and disorders; ability to multimerize; ability to bind a ligand; antigenic ability useful for production of polypeptide specific antibodies) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular

polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide as defined in columns 14 and 15 of Table 1A, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X or the complement thereof, a polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, a polypeptide encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1C, a polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or a mature polypeptide encoded by the cDNA contained in ATCC Deposit No:Z). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y, the mature (secreted) portion of SEQ ID NO:Y as defined in columns 14 and 15 of Table 1A, or the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

The present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, the mature (secreted) portion of SEQ ID NO:Y as defined in columns 14 and 15 of Table 1A, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, a polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, a polypeptide encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1C, a polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or a mature polypeptide encoded by the cDNA contained in ATCC Deposit No:Z). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and

where n corresponds to the position of amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y, the mature (secreted) portion of SEQ ID NO:Y as defined in columns 14 and 15 of Table 1A, and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), the cDNA contained in ATCC Deposit No:Z, and/or the complement thereof, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative diseases and disorders; ability to multimerize; ability to bind a ligand; antigenic ability useful for production of polypeptide specific antibodies) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

The present application is also directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence set forth herein. In preferred embodiments, the application is directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to polypeptides having the amino acid sequence of the specific N- and C-terminal deletions. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Any polypeptide sequence encoded by, for example, the polynucleotide sequences set forth as SEQ ID NO:X or the complement thereof, (presented, for example, in Tables 1A and 2), the cDNA contained in ATCC Deposit No:Z, or the polynucleotide sequence as defined in column 6 of Table 1C, may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ

ID NO:X (e.g., the polypeptide of SEQ ID NO:Y and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2) or the cDNA contained in ATCC Deposit No:Z may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; http://www.dnastar.com/).

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Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions; Chou-Fasman alpha-regions, beta-regions, and turn-regions; Kyte-Doolittle hydrophilic regions and hydrophobic regions; Eisenberg alpha- and beta-amphipathic regions; Karplus-Schulz flexible regions; Emini surface-forming regions; and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Preferred polypeptide fragments of the invention are fragments comprising, or alternatively, consisting of, an amino acid sequence that displays a functional activity (e.g. biological activity such as, for example, activity useful in detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating cancer and other hyperproliferative diseases and disorders; ability to multimerize; ability to bind a ligand; antigenic ability useful for production of polypeptide specific antibodies) of the polypeptide sequence of which the amino acid sequence is a fragment. By a polypeptide displaying a "functional activity" is meant a polypeptide capable of one or more known functional activities associated with a full-length protein, such as, for example, biological activity, antigenicity, immunogenicity, and/or multimerization, as described herein.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID

NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

#### Epitopes and Antibodies

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The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of: the polypeptide sequence shown in SEQ ID NO:Y; a polypeptide sequence encoded by SEQ ID NO:X or the complementary strand thereto; the polypeptide sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2; the polypeptide sequence encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1C or the complement thereto; the polypeptide sequence encoded by the cDNA contained in ATCC Deposit No:Z; or the polypeptide sequence encoded by a polynucleotide that hybridizes to the sequence of SEQ ID NO:X, the complement of the sequence of SEQ ID NO:X, the complement of a portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, or the cDNA sequence contained in ATCC Deposit No:Z under stringent hybridization conditions or alternatively, under lower stringency hybridization as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X, or a fragment thereof), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described *infra*. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Non-limiting examples of epitopes of polypeptides that can be used to generate antibodies of the invention include a polypeptide comprising, or alternatively consisting of, at least one, two, three, four, five, six or more of the portion(s) of SEQ ID NO:Y specified in column 6 of Table 1B.1. These polypeptide fragments have been determined to bear antigenic epitopes of the proteins of the invention by the analysis of the Jameson-Wolf antigenic index which is included in the DNAStar suite of computer programs. By "comprise" it is intended that a polypeptide contains at least one, two, three, four, five, six or more of the portion(s) of SEQ ID NO:Y shown in column 6 of Table 1B.1, but it may contain additional flanking residues on either the amino or carboxyl termini of the recited portion. Such additional flanking sequences are preferably sequences naturally found adjacent to the portion; i.e., contiguous sequence shown in SEQ ID NO:Y. The flanking sequence may, however, be sequences from a heterologous polypeptide, such as from another protein described herein or from a heterologous polypeptide not described herein. In particular embodiments, epitope portions of a polypeptide of the invention comprise one, two, three, or more of the portions of SEQ ID NO:Y shown in column 6 of Table 1B.1.

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient

to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies: according to methods well known in the art.

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As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention (e.g., those comprising an immunogenic or antigenic epitope) can be fused to heterologous polypeptide sequences. For example, polypeptides of the present invention (including fragments or variants thereof), may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof, resulting in chimeric polypeptides. By way of another non-limiting example, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused with albumin (including but not limited to recombinant human serum albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). In a preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with the mature form of human serum albumin (i.e., amino acids 1 - 585 of human serum albumin as shown in Figures 1 and 2 of EP Patent 0 322 094) which is herein incorporated by reference in its entirety. In another preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with polypeptide fragments comprising, or alternatively consisting of, amino acid residues 1-z of human serum albumin, where z is an integer

from 369 to 419, as described in U.S. Patent 5,766,883 herein incorporated by reference in its entirety. Polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused to either the N- or C-terminal end of the heterologous protein (e.g., immunoglobulin Fc polypeptide or human serum albumin polypeptide). Polynucleotides encoding fusion proteins of the invention are also encompassed by the invention.

Such fusion proteins as those described above may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin (HA) tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose column and histidinetagged proteins can be selectively eluted with imidazole-containing buffers.

#### Fusion Proteins

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Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

In certain preferred embodiments, proteins of the invention are fusion proteins comprising

an amino acid sequence that is an N and/or C- terminal deletion of a polypeptide of the invention. In preferred embodiments, the invention is directed to a fusion protein comprising an amino acid sequence that is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence of the invention. Polynucleotides encoding these proteins are also encompassed by the invention.

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Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

As one of skill in the art will appreciate that, as discussed above, polypeptides of the present invention, and epitope-bearing fragments thereof, can be combined with heterologous polypeptide sequences. For example, the polypeptides of the present invention may be fused with heterologous polypeptide sequences, for example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any combination thereof, including both entire domains and portions thereof), or albumin (including, but not limited to, native or recombinant human albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)), resulting in chimeric polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties (EP-A 0232 262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a polypeptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the

fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)).

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Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

# Recombinant and Synthetic Production of Polypeptides of the Invention

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by synthetic and recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and

late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418, glutamine synthase, or neomycin resistance for eukaryotic cell culture, and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Vectors which use glutamine synthase (GS) or DHFR as the selectable markers can be amplified in the presence of the drugs methionine sulphoximine or methotrexate, respectively. An advantage of glutamine synthase based vectors are the availability of cell lines (e.g., the murine myeloma cell line, NS0) which are glutamine synthase negative. Glutamine synthase expression systems can also function in glutamine synthase expressing cells (e.g., Chinese Hamster Ovary (CHO) cells) by providing additional inhibitor to prevent the functioning of the endogenous gene. A glutamine synthase expression system and components thereof are detailed in PCT publications: WO87/04462; WO86/05807; WO89/01036; WO89/10404; and WO91/06657, which are hereby incorporated in their entireties by reference herein. Additionally, glutamine synthase expression vectors can be obtained from Lonza Biologics, Inc. (Portsmouth, NH). Expression and production of monoclonal antibodies using a GS expression system in murine myeloma cells is described in

Bebbington et al., Bio/technology 10:169(1992) and in Biblia and Robinson Biotechnol. Prog. 11:1 (1995) which are herein incorporated by reference.

The present invention also relates to host cells containing the above-described vector constructs described herein, and additionally encompasses host cells containing nucleotide sequences of the invention that are operably associated with one or more heterologous control regions (e.g., promoter and/or enhancer) using techniques known of in the art. The host cell can be a higher eukaryotic cell, such as a mammalian cell (e.g., a human derived cell), or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. A host strain may be chosen which modulates the expression of the inserted gene sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristics and specific mechanisms for the translational and post-translational processing and modification (e.g., phosphorylation, cleavage) of proteins. Appropriate cell lines can be chosen to ensure the desired modifications and processing of the foreign protein expressed.

Introduction of the nucleic acids and nucleic acid constructs of the invention into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., the coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., US Patent Number 5,641,670, issued June 24, 1997; International Publication Number WO 96/29411; International Publication Number WO 94/12650; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite

chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolization pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O₂. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOXI*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOXI* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See Ellis, S.B., *et al.*, *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J, *et al.*, *Yeast* 5:167-77 (1989); Tschopp, J.F., *et al.*, *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOXI* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* 

alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino

acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

The invention encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include iodine (¹²¹I, ¹²³I, ¹²⁵I, ¹³¹I), carbon (¹⁴C), sulfur (³⁵S), tritium (³H), indium (¹¹¹In, ¹¹²In, ^{113m}In, ^{115m}In), technetium (⁹⁹Tc, ^{99m}Tc), thallium (²⁰¹Ti), gallium (⁶⁸Ga, ⁶⁷Ga), palladium (¹⁰³Pd), molybdenum (⁹⁹Mo), xenon (¹³³Xe), fluorine (¹⁸F), ¹⁵³Sm, ¹⁷⁷Lu, ¹⁵⁹Gd, ¹⁴⁹Pm, ¹⁴⁰La, ¹⁷⁵Yb, ¹⁶⁶Ho, ⁹⁰Y, ⁴⁷Sc, ¹⁸⁶Re, ¹⁸⁸Re, ¹⁴²Pr, ¹⁰⁵Rh, and ⁹⁷Ru.

In specific embodiments, a polypeptide of the present invention or fragment or variant thereof is attached to macrocyclic chelators that associate with radiometal ions, including but not limited to, ¹⁷⁷Lu, ⁹⁰Y, ¹⁶⁶Ho, and ¹⁵³Sm, to polypeptides. In a preferred embodiment, the radiometal ion associated with the macrocyclic chelators is ¹¹¹In. In another preferred embodiment, the radiometal ion associated with the macrocyclic chelator is ⁹⁰Y. In specific embodiments, the macrocyclic chelator is 1,4,7,10-tetraazacyclododecane-N,N',N",N"'-tetraacetic acid (DOTA). In other specific embodiments, DOTA is attached to an antibody of the invention or fragment thereof via a linker molecule. Examples of linker molecules useful for conjugating DOTA to a polypeptide are commonly known in the art - see, for example, DeNardo et al., Clin Cancer Res. 4(10):2483-90 (1998); Peterson et al., Bioconjug. Chem. 10(4):553-7 (1999); and

Zimmerman et al, Nucl. Med. Biol. 26(8):943-50 (1999); which are hereby incorporated by reference in their entirety.

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As mentioned, the proteins of the invention may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Polypeptides of the invention may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein

or analog). For example, the polyethylene glycol may have an average molecular weight of about 200, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10,000, 10,500, 11,000, 11,500, 12,000, 12,500, 13,000, 13,500, 14,000, 14,500, 15,000, 15,500, 16,000, 16,500, 17,000, 17,500, 18,000, 18,500, 19,000, 19,500, 20,000, 25,000, 30,000, 35,000, 40,000, 45,000, 50,000, 55,000, 60,000, 65,000, 70,000, 75,000, 80,000, 85,000, 90,000, 95,000, or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo et al., Appl. Biochem. Biotechnol. 56:59-72 (1996); Vorobjev et al., Nucleosides Nucleotides 18:2745-2750 (1999); and Caliceti et al., Bioconjug. Chem. 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, such as, for example, the method disclosed in EP 0 401 384 (coupling PEG to G-CSF), herein incorporated by reference; see also Malik et al., Exp. Hematol. 20:1028-1035 (1992), reporting pegylation of GM-CSF using tresyl chloride. For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e.,

separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems for attaching polyethylene glycol to proteins are described in Delgado et al., Crit. Rev. Thera. Drug Carrier Sys. 9:249-304 (1992); Francis et al., Intern. J. of Hematol. 68:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride (CISO₂CH₂CF₃). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoreothane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number of additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in International Publication No. WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (i.e., the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5,

4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado et al., Crit. Rev. Thera. Drug Carrier Sys. 9:249-304 (1992).

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The polypeptides of the invention can be recovered and purified from chemical synthesis and recombinant cell cultures by standard methods which include, but are not limited to, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification. Well known techniques for refolding protein may be employed to regenerate active conformation when the polypeptide is denatured during isolation and/or purification.

The polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer refers to a multimer containing only polypeptides corresponding to a protein of the invention (e.g., the amino acid sequence of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X or the complement of SEQ ID NO:X, the amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or an amino acid sequence encoded by cDNA contained in ATCC Deposit No:Z (including fragments, variants, splice variants, and fusion proteins, corresponding to these as described herein)). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing two polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing three polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a

heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotetramer.

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Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked by, for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or encoded by the cDNA contained in ATCC Deposit No:Z). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, osteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides

and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of

the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

#### **Antibodies**

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Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of the invention (e.g., a polypeptide or fragment or variant of the amino acid sequence of SEQ ID NO:Y or a polypeptide encoded by the cDNA contained in ATCC Deposit No:Z, and/or an epitope, of the present invention) as determined by immunoassays well known in the art for assaying specific antibody-antigen binding. Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), intracellularlymade antibodies (i.e., intrabodies), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. In preferred embodiments, the immunoglobulin molecules of the invention are IgG1. In other preferred embodiments, the immunoglobulin molecules of the invention are IgG4.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal



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